192617

From:

Jiang, Dong

Sent:

Monday, June 12, 2006 6:34 PM

To: Subject: STIC-Biotech/ChemLib 10/797,157

Please search SEQ ID NO:2 (aa, standard & oligomer search)

- issued & Pub.
- commercial

Please send results on paper to Dong Jiang in REM 4D70 (mail stop REM 4C70).

Thank you very much.

Dong

Dong Jiang

AU1646 REM - 4D70 571-272-0872 Mail stop REM - 4C70

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search

NA#_____AA#:___
S/L:___Oligomer:___
Encode/Transl:___
Structure #:____Text:__
Inventor:____ Litigation:___

Vendors and cost where applicable STN:

DIALOG:
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SEQUENCE SYSTEM:
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GenCore version
Copyright (c) 1993 - 2006
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Listing first 45 summaries
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ALIGNMENTS

AAW95002 standard, protein, 189 AA

AAW95002

Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation; inflammatory condition; drug screening; human. Human interleukin-B30 (IL-B30) polypeptide. 1. .21 /note= "signal peptide" 22. .189 /note= "mature protein" Location/Qualifiers 98WO-US015423. 97US-00900905. (first entry) (SCHE) SCHERING CORP. WPI; 1999-142935/12. N-PSDB; AAX17786. 21-MAY-1999 Homo sapiens 24-JUL-1998; 25-JUL-1997; WO9905280-A1 04-FEB-1999, Bazan JF; AAW95002; Protein Peptide Key

Newly isolated or recombinant polynucleotide encoding mammalian cytokine interleukin-B30 (IL-B30), including fragments - useful for regulating activation, development, differentiation and function of various cell types, and for diagnosing and treating conditions associated with IL-B30.

Claim 2; Page 8-9; 83pp; English.

This represents a human cytokine interleukin-B30 (IL-B30) polypeptide. Host cells containing a vector comprising the IL-B30 nucleic acid are used for the recombinant production of the protein. The polynucleotides

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receptor subunits useful in the treatment inflammatory disorders
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 are useful for diagnosis of IL-B30 mediated conditions, and forensic science (e.g. to distinguish rodent from human, or as a marker to distinguish between different cells exhibiting differential expression or modification patterns). The IL-B30 (including fragments), together with antibodies that bind to IL-B30 are useful for teaching purposes. They are also used for treating conditions associated with abnormal physiology or development, including inflammatory conditions. The polypeptide cytokine should mediate cytokine synchesis and proliferation in cells. IL-B30 is useful for drug screening to identify compounds having binding affinity
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100.0%; Pred. No. 6.2e-97;
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/label= signal
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N-PSDB; AAZ08865.
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Subunit I (DERSI) protein and DNAK Soluble receptor subunit I (DERSI) protein and DNAK Soluble receptor subunit I (DERSI) protein, which together encode a new mammalian cytokine recaptor (R), or DERSI and interleukin B30 (IL-B30) proteins, or DERSI and interleukin B30 (IL-B30) proteins, or DERSI and interleukin B30 (IL-B30) proteins, or screening for ligands (I.e. agonists/antagonists) from a library of compounds, which are useful for modulating the physiology or development of a cell or tissue culture e.g. inflammatory responses, innate immunity and/or morphogenic development. (R), antibodies and ligands are useful for treatment of conditions, especially immunological disorders, associated with conditions exhibiting abnormal expression of (R). (R) is useful as a phosphate labeling enzyme to label substrates, and the subunits DERSI and DERSI are useful as immunogens for generating (R) are useful for identifying related DNAs and mRNAs, and wariants from the are useful for identifying related DNAs and man variants from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other individuals or species. The present sequence represents the specifically claimed human IL-B30, for use in the composition of the
                                                                      present invention describes a composition (I) comprising DNAX
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/note= "Signal peptide"
Claim 2; Page 26-27; 133pp; English.
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                                                                                                                                                                                                                This sequence represents human interleukin-B30 (IL-B30). IL-B30 is a novel cytokine, exhibiting significant homology to IL-6 and GCSF (granulocyte colony stimulating factor). Cytokines play a critical role in signalling between immune or other cells during an immune response. The precise role if IL-B30 is not yet known - it is likely to have either a stimulatory or an inhibitory effect on haematopoietic cells such as T-cells, B-cells, natural killer (NK) cells and macrophages. Alternatively, it may affect vascular physiology or development, or have neuronal effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and antagonists are useful in the diagnosis and treatment of disorders associated with abnormal expression or activity of IL-B30 e.g., inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are useful for recombinant expression of IL-B30 in a host cell, and as a source of probes and primers. The IL-B30 probes and primers can be used: to detect levels of IL-B30 expression in samples from patients suspected of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may also be used to identify homologous genes in other species. IL-B30 protein or its fragments are useful as antigens for raising antibodies to various linear and conformational epitopes. Such antibodies may be used to detect levels of IL-B30 protein in a sample
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                                                                                                                                          Novel recombinant DNA encoding cytokines especially interleukin-B30 useful as probes or primers for diagnosing immune disorders including autoimmune or chronic inflammatory conditions.
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0
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 98US-00122443
                         97US-0053765P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 189; Conservative
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                                                   (SCHE ) SCHERING CORP.
                                                                                                   WPI; 2000-364420/31.
N-PSDB; AAA52577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 189 AA;
 24-JUL-1998;
                        25-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUN-2001
                                                                            Bazan JF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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This sequence shows human interleukin-B30. Fragments of this protein may be used in the composition of the invention. The composition comprises a substantially pure polypeptide comprising a number of distinct segments of at least 7 contiguous amino acids from IL-12 p40 and/or IL-B30, and a substantially pure polypeptide comprising a segment of at least 11 contiguous amino acids from IL-12 p40 and/or IL-B30. The composition is useful for modulating physiology or development of a cell or tissue in a host organism, resulting in an increased or decreased production of interferon-gamma (IFNgamma), an enhanced Thi response such as anti-tumour effect, and amelioration of an autoimmune condition or a chronic configuration of memory T-cells. An agonist is useful inducing the proliferation of memory T-cells. An agonist is useful for modulating he trafficking or activation of a leukocyte in an animal experiencing science or symptoms of autoimmunty, leukocyte in an animal experiencing science or symptoms of autoimmunty.
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memory T-cell; leukocyte; rheumatoid arthritis; osteoarthritis; atherosclerosis; multiple sclerosis; vasculitis; spinal injury; delayed hypersensitivity; skin graft; transplant; cancer; tumour; stroke; neurodegeneration; ischaemia; postmenopausal osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESTTNDVPHIQCGDGCDPQGLRDNSQFCLQRİHQCLIFYEKLLGSDIFTGEPSLLPDSP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition comprising interleukin-12 p40 and IL-B30 polypeptide or ite segment, useful for ameliorating rheumatoid arthritis, osteoarthritis, atherosclerosis, multiple sclerosis, vasculitis and tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MIGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       De Waal Malefyt R, Rennick DM, Kastelein RA;
", Lira SA, Narula SK;
                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Signal peptide"
22. .189
/note= "Mature protein"
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                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
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99US-0164616P.
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N-PSDB; AAC85540.
                                                                                                                                                                            Castleman's disease.
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Length 189, Indele 9 9

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ABU08268

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                                                                                                                                                                                                                  61 DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
                                                                                                                                                                                                                                                                     Human, antigenic, cytokine, interleukin-B30, IL-B30, protein therapy,
inflammatory condition, autoimmune disorder, activation, development,
differentiation, function, haematopoietic cell; lymphoid cell; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention discloses an isolated antigenic mature polypeptide that is a mammalian cytokine designated interleukin-B30 (IL-B30). The IL-B30 polypeptide is useful for diagnosing or treating (e.g. protein therapy) conditions associated with abnormal physiology or development (e.g. inflammatory conditions or autoimmune disorders), or in regulating the activation, development, differentiation and function of haematopoietic
                                                                                                                                     1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
                                                                                                 1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
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                 Score 1004; DB 6;
Pred. No. 6.2e-97;
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                                                           0; Mismatches
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/label= Signal_peptide
22. .189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiinflammatory; immunosuppressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG75811 standard; protein; 189 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human interleukin-B30 (IL-B30).
                 100.0%;
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98US-00122443.
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                                                           Matches 189; Conservative
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N-PSDB; ABX11988.
               Query Match
Best Local Similarity
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24-JUL-1998;
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                                                              DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22. .189
/label= Mature_IL_B30
/note= "This protein is specifically claimed in claim 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Binding compounds comprising antibodies which bind to Interleukin B30, useful for treating disorders associated with hematopoietic cells, e.g. inflammation and autoimmune diseases and development disorders.
                                       VAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVF
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; interleukin-B30; IL-B30; inflammation; lymphoid cell; immunosuppressive; autoimmune disorder; immunomodulatory; autoimmune autoimmune autoimmune autoimmune autoimmune tory; vascular; neuroprotective; immunological response; haematopoietic cell disorder; vascular physiology; development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .21
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                            ABU08268 standard; protein; 189 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                        Human interleukin-B30, IL-B30,
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98US-00122443.
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24-JUL-1998;
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Peptide Protein

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Bazan JF;

RESULT 5
ABU09368
ID ABU09368
XX ABU0936
XX Huma Immu
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Sequence 189 AA;

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WO2004058178-A2
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cells or lymphoid cells. The IL-B30 polypeptide is also useful as an immunogen for producing antisera or antibodies specific for binding. The sequence presented is the human IL-B30 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; interleukin B30; IL-B30; IL-12 p40; tumour necrosis factor alpha; IRN-alpha; interferon alpha; chronic inflammatory condition; memory T-cell; tumour, anti-viral; vaccine; allergic responses; autoimmune disease; multiple sclerosis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition comprising fragments from interleukin (IL)-12 p40 and IL-B30 polypeptides is useful to enhance anti-viral, anti-tumor and vaccine effects and to antagonize allergic responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a composition comprising polypeptide fragments from interleukin (IL)-12 p40 and IL-B30 is new. The fragments comprise 7 or 11 contiguous amino acids. Also included are an isolated or recombinant nucleic acid (N1) encoding the polypeptides of the novel
                                                                                                                                                                                                                                                                                                                                                                                                    121 VAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVARVF
                                                                                                                                                                                                             MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
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                                                                                                                              Length 189;
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                                                                                                                                                                   Indels
                                                                                                                              DB 6;
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                                                                                                                          100.0%; Score 1004; DB 6;
100.0%; Pred. No. 6.2e-97;
ive 0; Mismatches 0;
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T, Lira SA, Narula SK;
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10-NOV-1999; 99US-0164616P.
08-SEP-2000; 2000US-00658699.
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                                                                                                                   Query Match
Best Local Similarity 100.
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human interleukin B30.
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N-PSDB; ADF70611.
                                                                                     Sequence 189 AA;
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Wiekowski MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Composition, a cell comparising recombinant NI, a nuclear acid which composition, a cell comparising period of combined with a tumour necrosis factor (TNF) alpha antagonist, in IL-12 antagonist, IL-10 or steroids), a children composition of IL-12 p40/IL-B30 (combined with a tumour necrosis binding compound comprising an antigen binding site from an antibody which specifically binds to the novel composition, producing an antigen binding site from an antibody or development of antigen: antibody complex, modulating physiology or development of conficient of IPN-alpha, modulating physiology or development of conficient of IPN-alpha, modulating physiology or development of conficients of IPN-alpha, modulating physiology or development of conficients of IPN-alpha, modulating physiology or development of comprising conficients and anti-tumour, adjuvant, anti-viral or antagonised conficients of an anti-tumour, adjuvant, anti-viral or antagonised condition of an autoimmune condition or a chronic inflammatory response condition, increasing secretion of a primate IL-B30 (comprising expressing IL-B30 with IL-I2 p40 with IL-B30, screening for a receptor which binds the novel composition, modulating the inflammatory response comprising expressing IL-B30 or its agonist. The invention is useful in administering IL-B30 or its agonist. The invention is useful in antimal and inducing the proliferation of memory 7-cells by administering IL-B30 or its agonist. The invention is useful in antimal and caeching. They are useful to treat autoimmune diseases such as multiple sclerosis or particularly the complex is useful to enhance anti-tumour, anti-viral and caeching the proliferation and caeching including inflammatory conditions. Particularly the complex is useful to enhance anti-tumour, anti-viral and caeching the complex associated with abnormal physiology including inflammatory conditions. Particularly the complex is useful to enhance such as multiple sclerosis or inflammatory bowel disease. The present sequence represents human I
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a cell comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .21
/note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Mature protein"
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Matches 189; Conservative
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Peptide
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                                                                                                                                                                                                                             healing. The method comprises administering to a subject an agonist or an agonist or an agonist of intergleukin (IL)-23. The invention further comprises; an agonist of IL-23 derived from the binding site of an antibody that specifically binds to an IL-23 receptor; and a kit comprising the agonist and a compartment or instructions for use or disposal. The interleukin-23 agents have vulnerary activity. The method is useful for treating or improving wound healing. This sequence represents a cytokine human interleukin-19 protein used in the wound healing method of the invention.
                                                                                                                                                           Treating inflammatory skin disorders or improving wound healing comprises administering to a subject an agonist or antagonist of Interleukin-23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEETTINDVPHIOCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVF 180
                                                                                                                                                                                                                                                                                                                                                                                                                     1 MIGSRAVMILILIDWIAQGRAVPGGSSPAWIQCQQLSQKLCTLAWSAHPLVGHMDLREEG 60
                                                                                                                                                                                                                     The invention relates to a novel method for treating or improving wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; interleukin 23; subunit p19; IL-23; IL-23p19; tumour; growth; agonist; antagonist; receptor; cancer; antigen-binding site; antibody; extracellular region; antisense nucleic acid; small interference RNA; spiRNI) polyclonal; monoclonal; humanized; Fab; Fv; F(ab')2; peptide mimetic; colon; ovarian; breast; melanoma; cachexia; anglogenesis; gastrointestinal tract; respiratory tract; reproductive system; endocrine system.
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                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1004; DB 8; Length 189; 100.0%; Pred. No. 6.2e-97; ive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                              Example; SEQ ID NO 4; 52pp; English
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                                18-DEC-2003; 2003WO-US040937
                                                       23-DEC-2002; 2002US-0436274P
                                                                                                     Cua DJ;
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Best Local Similarity 100.
Matches 189; Conservative
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                                                                              (SCHE ) SCHERING CORP
                                                                                                                          WPI; 2004-525781/50.
N-PSDB; ADQ14468.
                                                                                                   Chen S,
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                                                                                                     Bowman EP,
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This sequence represents human interleukin 23 subunit p19 (IL-21p19). The method of the invention for modulating tumour growth comprises contacting a tumour cell with an agonist or antagonist of IL-23. The agonist or artagonist is a binding composition which specifically binds the IL-23 opinist or antagonist may be used for diagnosition The identified agonist or the IL-23 receptor (IL-21R) protein. The identified subject suffering from a cancer or tumour. The binding or treating a subject suffering from a cancer or tumour. The binding or modular region of IL-21R, a small molecule, an antisense nucleic acid or small interference RNA (siRNA), or a detectable label. The binding composition comprises a polyclonal antibody, a monoclonal antibody, a humanized antibody or its fragment, a Pab, Pv, Fab') 2 fragment, or a peptide mimetic of an antibody. The tumour cell is a colon, ovarian or breast cancer cell, or melanoma cell. In the treatment method, the antagonist of IL-23 inhibits growth of cancer or tumour, cachexia, anorexia or angiogenesis. The cancer or tumour is of the gastrointestinal tract, respiratory tract, teproductive system or endocrine system. In diagnosing cancer or tumour, the binding composition comprises a nucleic acid probe or primer that specifically binds or hybridises to human or mouse IL-23p19 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modulating tumor growth, useful for treating a subject suffering from cancer or tumor, comprises contacting a tumor cell with an agonist or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapв
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                                                                                                 /note= "Mature IL-23p19"
                            "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; SEQ ID NO 2; 57pp; English.
                                                                                                                                                                                                                                                                                                                   09-MAR-2004; 2004WO-US007198
                                                                                                                                                                                                                                                                                                                                                                                     10-MAR-2003; 2003US-0453672P
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Matches 189; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mcclanahan TK;
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N-PSDB; ADS73600.
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ADV98151 standard; protein; 189 AA.

ADV98151

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Location/Qualifiers

protein.

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The present invention relates to a method of treating a human subject experiencing a physiological disorder. The method involves administering an agonist or antagonist of DNAX cytokine receptor subunit 5 (DCRS5, also Known as IL-23R) or of pl9, where the disorder comprises asthma or allergy, chronic obstructive pulmonary disorder (COPD) or an interstitial lung disorder. The invention is useful for treating interstitial lung disorder e.g. idiopathic pulmonary fibrosis, eosinophilic granuloma and hypersensitivity pneumonitis. The present sequence is the human pl9
 121 VAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of an agonist or antagonist of DNAX cytokine receptor subunit 5 (DCRS5) or of p19 for treating a human subject experiencing a physiological disorder such as allergy or chronic obstructive pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 VAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVF
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                                                                                                                                                                                                                                                                                     Diagnosis; therapeutic; asthma; antiasthmatic; immune disorder; infilamation; respiratory disease; allergy; antiallergic; chronic obstructive pulmonary disease; respiratory-gen.; pulmonary fibrosis; antiinflammatory; pneumonia; infection; p19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1004; DB 9; Length 189; 100.0%; Pred. No. 6.2e-97; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moore KW, Parham CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 6; 89pp; English.
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                                                                                                                                                   AEA51094 standard; protein; 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-NOV-2004; 2004WO-US038886.
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                                                                                                                                                                                                                     (first entry)
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                                 AHGAATLSP 189
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                                                               AHGAATLSP
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                                                                                                                                                                                                                                                     Human p19 protein.
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                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of detecting (MI) a polynucleotide, by contacting a polynucleotide with a probe (PB) that hybridizes, under stringent wash conditions to at least 134 or 25 contiguous nucleotides of open reading frame of a fully defined interleukin (IL)-B30 sequence of duplex indicates presence of polynucleotide. The method is useful for detecting the expression of IL-B30 polynucleotide, and for detecting the expression of IL-B30 polynucleotide, and for detecting levels of IL-B30 polynucleotide, and for detecting levels of IL-B30 polynucleotide, and for detecting levels of IL-B30 in samples from patient suspected of having abnormal conditions such as inflammatory or autoimmune. The method is also useful in forensic science, e.g. to distinguish rodent from human or to distinguish between different cell exhibiting differential expression or modification different associated with abnormal expression or signaling by IL-B30. This sequence corresponds to the novel interleukin-B30 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting interleukin-B30 polynucleotide, comprises contacting polynucleotide with probe capable of hybridizing with contiguous nucleotides of polynucleotide to form duplex, where detection of duplex
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                                                                                                                DNA purification, cytokine; interleukin-B30; IL-B30; inflammation; autoimmune disorder; forensic science; differential expression.
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; Pred. No. 6.2e-97;
0; Mismatches 0;
                                                                                                                                                                                                                                                                   /note= "mature IL-B30 protein"
                                                                                                                                                                                                                    1. .21
/note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              indicates presence of polynucleotide.
                                                                                Novel human interleukin B30 protein.
                                                                                                                                                                                                    Location/Qualifiers
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98US-00122443.
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N-PSDB; ADV98150, ADV98152.
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Best Local Similarity 100.
Matches 189; Conservative
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                                                                                                                                                                    Homo sapiens
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24-JUL-1998;
                                                 10-MAR-2005
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              ADV98151;
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AAA16618 to AAA16697 encode the human secreted proteins given in AAY94898 to AAA16697, isolated from human adult brain, adult thyroid, adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney, adult placenta, adult testis, whole embryo, adult cartilage, kidney, foetal brain, adult thymus, foetal placenta, adult userus, adult tumour, and adult bladder, cDNA libraries. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliocating medical conditions in humans and animals. The polynucleotides can be used as markers for tissues in which the protein is preferentially expressed, as molecular weight markers on Southern gels, and as chromosome markers or tags to identify chromosomes
antibacterial; antifungal; cytostatic; antiinflammatory; dermatological; antidiabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide; antithyrold; immune deficiency; severe combined immunedeficiency; SCID; infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus; connective tissue disease; multiple sclerosis; erythematosis; heumatoid arthritis; autoimmune pulmonary inflammation; asthma; duillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis; insulin dependent diabetes mellitus; graft-versus-host-disease; autoimmune inflammatory eye disease; allergy.
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                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; immunestimulant; immunesuppressant; virucide;
                                                                                                                                                                                                                                                                                                                     Human secreted protein clone rk80_3 protein sequence SEQ ID NO:138
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Spaulding
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Steininger RJ, S
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1, Agostino MJ,
Fechtel K;
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                                                                                                                                                                                                       AAY94966 standard; protein; 189 AA.
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98US-0096815P.
98US-0109229P.
98US-010534P.
99US-0119931P.
99US-0120575P.
99US-0132020P.
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12-FEB-1999;
18-FEB-1999;
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Wong GG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated or recombinant polynucleotide encoding an antigenic interleukin-B30 (IL-B30), useful in diagnostic applications for IL-B30 mediated conditions such as inflammatory conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Mature human interleukin-30 (IL-B30) protein"
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drug screening; inflammation; antiinflammatory.
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                                                                                                                                                                                                                                                                                    Human interleukin-B30 (IL-B30) protein, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .21
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                              AEB47331 standard; protein; 189 AA.
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                                               AHGAATLSP 189
                        AHGAATLSP 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel cytokine-like protein, with activity of supporting proliferation of myeloid cells, useful in treating abnormality of cell proliferation in immune and hematopoiesis systems.
                                                                                                                                                                                                                                                                                 DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
                                                                                                                                                                                                                                                                                                                               VAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVF 180
or to map gene positions. The proteins can be used in the treatment of immune deficiencies and disorders, such as severe combined immunedeficiency (SCID), as well as viral, bacterial, fungal and other infections. These infections include human immunodeficiency virus. (HIV), hepatitis, herpesviruses, mycobacteria, Leismania spp., malaria and candidiasis. The proteins can be used to treat autoimmune disorders such as connective tissue disease, multiple sclerosis, systemic lupus erythematosis, rheumatoid arkbritis, autoimmune pulmonary inflammation, diabetes mellitus, myasthenia gravis, graft-versus-host-disease and autoimmune inflammatory eye disease. The proteins can also be used to treat allergic conditions, such asthma. AAA16698 to AAA1674 represent probes for the human secreted proteins from the present invention
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                                                                                                                                                                                                                                                  MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQXLCTLAWSAHPLVGHMDLREEG
                                                                                                                                                                                                                                                                                              VGOLHASLLGLSOLLOPEGHHWETQOIPSLSPSOPWORLLLRFKILRSLOAFVAVARVF
                                                                                                                                                                                                                                      1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor; cell proliferation;
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                                                                                                                                                                                     Query Match 99.6%; Score 1000; DB 3; Length 189; Best Local Similarity 99.5%; Pred. No. 1.6e-96; Matches 188; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune system; haematopoietic system; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G-CSF related
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAYS4606 standard; protein; 189 AA.
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N-PSDB; AAZ37262, AAZ37263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein sequence
                                                                                                                                                                 Sequence 189 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
This sequence is the Interleukin-6 G-CSF related factor (SGRP) protein of the invention. The protein is a member of the IL-6/G-CSF/MSF family. The protein can be used in drugs for treating diseases due to abnormality of cell proliferation in the immune system and haematopoietic system
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                                                                                                                                                                                                                                    DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP
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                                                                                                                                                                                                                                                                                                                                                                                      MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
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                                                                                                                                    Length 189;
                                                                                                                                                                      1; Indels
                                                                                                                                  Score 1000; DB 3;
Pred. No. 1.6e-96;
0; Mismatches 1;
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99WO-US030999.
99WO-US031243.
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99WO-US028551
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2000WO-US005601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-OCT-2001 (first entry)
                                                                                                                                    Query Match 99.6
Best Local Similarity 99.5
Matches 188; Conservative
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                                                                                                Sequence 189 AA;
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06-JAN-2000;
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02-MAR-2000;
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22-FEB-2000;
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Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G:
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                               Claim 12; Fig 232; 813pp; English
                        20-MAR-2000; 2000W0-US007377.

21-MAR-2000; 2000W0-US007532.

30-MAR-2000; 2000W0-US018439.

17-MAY-2000; 2000W0-US0114042.

22-MAY-2000; 2000W0-US014041.

02-JUN-2000; 2000W0-US01564.

05-JUN-2000; 2000W0-US01564.

05-JUN-2000; 2000W0-US020812P.

28-JUL-2000; 2000W0-US020812P.
                                                                                                            11-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US03328.
08-NOV-2000; 2000WO-US030952.
                                                                                                                                                10-NOV-2000; 2000WO-US030873
                                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                        2001-408281/43.
                                                                                                                                                                                                                               N-PSDB; AAS21359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 189 AA;
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g à ANU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to alink bloactive molecules to calls expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, persent, rectal, cervical or liver tunours by comparing PRO polypeptide expression in a call sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNP-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation of proliferation of inner ear utricular supporting cells or of T proliferation of inner ear utricular supporting cells or of the PRO prolypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or thinbit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polymetides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung, breast, prostate, cervical. Gao W;

DEETTINDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120

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99.6%; Score 1000; DB 4; Length 189; 99.5%; Pred. No. 1.6e-96; tive 0; Mismatches 1; Indels 0

Best Local Similarity 99.5 Matches 188; Conservative

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Query Match

61 DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120

VAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVF 180

Search completed: June 20, 2006, 04:32:11 Job time : 301.555 secs 181 AHGAATLSP 189

181 AHGAATLSP 189

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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sw model - protein search, using OM protein

Run on:

June 20, 2006, 04:32:40; Search time 25.0364 Seconds (without alignments) 726.342 Million.cell updates/sec

Title: Perfect score:

US-10-797-157-2 1004 1 MLGSRAVWLLLLLPWTAQGR......QAFVAVAARVFAHGAATLSP 189 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries Post-processing: Minimum Match 100 Maximum Match 100% Listing first 45 sm

Database :

PIR 80:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		granulocyte colony	granulocyte colony	•		granulocyte colony	granulocyte colony	exodeoxyribonuclea	interleukin-6 prec		hypothetical prote	taste receptor TIR	myelomonocytic gro	aerotaxis receptor	enoyl-[acyl-carrie	hypothetical prote	conserved hypothet	hypothetical prote	N-acetyl-glucosami	valyl-tRNA synthet	molybdopterin oxid	granulocyte colony	probable enoyl-CoA	chromatin assembly	probable acetyl-Co	interferon omega -	interleukin-6 prec	glucose dehydrogen	hypothetical prote	interleukin 6 - pi
	Ę		FOHUGE	T09255	S29549	T10268	A24573	A26496	A82809	ICMS6	D70537	D96810	JC7683	A42247	AG0893	XYCHFA	T05882	C82366	G86229	AI1929	F84404	A84240	JC5043	B83395	A56731	T07920	I47070	A34247	S00943	T48107	146590
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de	Query		10.0	6.6	9.1	9.0	8.8	8.7	9.8	8.5	8.0	8.0	8.0	7.9	•	7.9	7.8	7.7	7.7	7.6	7.6	7.6		7.5	•	7.5	7.5	7.5	7.5	7.5	7.4
	94000		100	99.5	91	90.5	88.5	87.5	98	82	80.5	80.5	80	79.5	79	79	78	77.5	77.5	76.5	76.5	92	75.5	75.5	75.5	75.5	75	75	75	75	74.5
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prointerleukin 6 -	hypothetical prote	hypothetical prote .	hypothetical prote	F13K23.18 protein	transcription-repa	probable glucose-6	probable glutamina	probable glutamina	probable protein k	photoreceptor - De	beta-galactosidase	testosterone-resis	UDP-N-acetylmuramo	class II histocomp	oligopeptide ABC t
146621	S75845	T27137	T26739	A86263	AD0198	H70916	B90696	F85546	T04005	D75598	139697	A58583	AI2319	T28147	C98215
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212	280	314	374	974	1148	247	310	310	649	755	1015	346	462	259	374
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ALIGNMENTS

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granulocyte colony-stimulating factor precursor - human N; Alternate names: colony-stimulating factor 3; G-CSF

C;Species: Homo sapiens (man) C;Date: 30-Jun-1988 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004 C;Accession: A25093; A49796; A47587; S68331

R.Nagata, S.; Tsuchiya, M.; Asano, S.; Yamamoto, O.; Hirata, Y.; Kubota, N.; Oheda, M.; EMBO J. S, 575-581, 1986 A.Title: The chromosomal gene structure and two mRNAs for human granulocyte colony-stim

A,Title: The chromosomal gene structure and two mRNAs for human granulocyte colony-stimm A,Reference number: A25093; MUID:86220137; PMID:2423327

A; Molecule type: DNA; mRNA A; Accession: A25093

A, Residues: 1-204 cNAC>
A, Residues: 1-204 cNAC>
A, Cross-references: UNIPROT: P09919; UNIPARC: UP1000002A734; EMBL: X03656; EMBL: X03655; NII
R, Devlin, J.J.; Devlin, P.E.; Myambo, K.; Lilly, M.B.; Rado, T.A.; Warren, M.K.
J. Leukoco. Biol. 41, 302-306, 1987
A, Title: Expression of granulocyte colony-stimulating factor by human cell lines.
A, Reference number: A49796; MUID: 87196936; PMID: 3494801

A; Molecule type: mRNA A; Accession: A49796

A;Cross-references: UNIPARC:UP1000002A734; GB:M17706; NID:g183040; PIDN:AAA35882.1; PID R;Souza, L.M.; Boone, T.C.; Gabrilove, J.; Lai, P.H.; Zsebo, K.M.; Murdock, D.C.; Chazi. A; Residues: 1-204 <DEV>

Science 232, 61-65, 1986
A;Title: Recombinant human granulocyte colony-stimulating factor: effects on normal and A;Reference number: A47587; MUID:86151684; PMID:2420009
B:MA1000010:: A47587

A; Molecule type: mRNA A; Residues: 19-204 < SOU.> A; Residues: 19-204 < SOU.> A; Cross-references: UNIPARC: UP10000158376; GB: M13008; NID: 9183044; PIDN: AAA03056.1; PID R; Haniu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F. R; Haniu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F. A; Haniu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F. A; Hitle: Extracellular domain of granulocyte-colony stimulating factor receptor. A; Reference number: S68331; MUID: 96132662; PMID: 8554326

A;Molecule type: protein A;Residues: 'M',31-46 <HAN> A;Cross-references: UNIPARC:UP10000173677

A,Gene: GDB:CSF3

A, Cross-references: GDB:119083; OMIM:138970

A,Map position: 17q11.2-17q12 A;Introns: 14/1; 65/3; 101/3; 150/3

A.Description: stimulates the differentiation and proliferation of hematopoletic progen: C,Superfamily: interleukin-6

C;Superfamily: interleukin-6 C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer P;1-130/Domain: signal sequence #status predicted <SIG> F;31-204/Product: granulocyte colony-etimulating factor #status predicted <MAT> F;66-72,94-104/Disulfide bonds: #status predicted

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hematopoietic progeni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T10268
R;O'Brien, P.M.; Seow, H.F.; Rothel, J.S.; Wood, P.R.
DNA Seq. 4, 339-342, 1994
A;Title: Cloning and sequencing of an ovine granulocyte colony-stimulating factor
A;Reference number: Z17009; MUID:95102116; PMID:7528579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 QRIHQGLIFYEKLLGSDIFTG-EPSLLPDSPVAQLHASLLGLSQLLQPEGHHWETQQIPS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 DOLHGGLFLYQGLL--QALAGISPELAPTLDTLQLDVTDFATNIWLQMB----DLGVAPA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 QNEFEGN-----QETVMELQSSIRTLIQILKEKIAGLITTPATH---TDLLEKMQSSNEW 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Č;Species: Ovis orientalis arīes, Ovis ammon aries (domestic sheep)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 ELQERLCATHKLCHPEELVLLGH-----SLGIPQAPL-SSCSSQSLQLTS--CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 AVSLGLLLVMTS-AFPTPGPLGEDFKNDTTPSRLLLTTPEKTEALIKHIVDKISAIRKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 REEGDE-----ETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 SDIFTGEPSLLPDSPVAQLHASLLGLSQLLQ-----PEGHHWETQQIPSLSPSQPW
                                                                                                                                                                                                                                                                                                                                                                                         6 AVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHM-----DL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 QLSQKLCTLAWSAHP----LVGHMDLREEGDEETTNDVPHIQCGDGCDPQGLRDNSQFCL
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
A;Accession: S29549
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-208 <EBR>A;Cessidues: 1-208 <EBR>A;Cessidues: UNIPARC:UPI000017366D; EMBL:X68723
C;Superfamily: interleukin-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
                                                                                                                                                                                                                                                                                                                   40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Description: stimulates the differentiation and proliferation C, Superfamily: interleukin-6 C, Keywords: cytokine; growth factor; macrophage
                                                                                                                                                                                                                                              Length 208
                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - sheep (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 LSPSQ-----PWQRLLLRFKILRSLQAFVAVAAR 178
                                                                                                                                                                                                                                              Query Match 9.1%; Score 91; DB 1; Les
Best Local Similarity 24.8%; Pred. No. 0.37;
Matches 50; Conservative 25; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-174 <OBR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 QRLLLRFKILRSLQAFVAVAAR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  granulocyte colony-stimulating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 granulocyte colony-stimulating factor precursor - cat (fragment)
C;Species: Felis silvestris catus (domestic cat)
C;Species: 1-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T0955
R;Dunham, S.P.; Onions, D.E.
R;Dunham, S.E.; Onions, D.E.
R;Dunham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Residues: 1-194 <DUN>
A;Residues: 1-194 <DUN>
A;CBORTION:
C;Function:
A;Description: stimulates the differentiation and proliferation ofhematopoietic progenit
C;Superfamily: interleukin-6
C;Kuperfamily: interleukin-6
C;C;Keyords: cytckine; growth factor; macrophage
F;1-20/Domain: signal sequence (fragment) #status predicted <SIG>F;1-20/Domain: signal sequence (fragment) #status predicted <MAT>
                                                                            11;
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                                                                                                                                                                                                                                                                                                                              55 DLREEGDEETTUDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTG-EP 113
                                                                                                                                                                                                                                                                                                                                                                                                                              114 SLLPDSPVAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQ------PWQRLLLRFKI 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | | | | | | | CHPEELVLIGH------ALGIPQAPL-SSCSSQALQLTG--CLRQLHSGLFLYQG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 AHP----LVGHMDLREBGDEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLGSDIFTG-EPSLLPDSPVAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQ----- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 LL--QALAGISPELAPTLDMLQLDITDFAINIWQQME----DVGMAPAVPPTQGTMPTFT 161
                                                                                                                                              ---LSQKLCTLAWSAHP----LVGHM 54
                                                                                                                                                                                       7 VMLLLLLPWTAQ----GRAVPGGSSPAWTQ-----CQQ------LSQKLCTLAWS 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LMALQLLLWHSALWMVQEATPLGPTSSLPQSFLLKCLEQVRKVQADGTALQERLCAAHKL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interloukin-6 - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis Ospecies (Species)
C;Accession: S29549
R;Ebrahimi, B.
Submitted to the EMBL Data Library, October 1992
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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9.9%; Score 99.5; DB 2; Length 194;
Best Local Similarity 23.9%; Pred. No. 0.055;
Matches 50; Conservative 27; Mismatches 79; Indels 53
       Length 204;
   10.0%; Score 100; DB 1; Length 20.
25.9%; Pred. No. 0.052;
ive 20; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAFQRRAGGTLVASNLQSFLEVAYRALRH 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 - PWQRLLLRFKILRSLQAFVAVAARVFAH 182
                                                                                                                                              15 WTAQGRAVPGGSSPAWTQ----CQQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRSLOAFVAVAARVFAH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||:|: |: || |
184 ASHLQSFLEVSYRVLRH 200
                                                                            51; Conservative
                                        Similarity
   Query Match
Best Local S:
Matches 51
                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103
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PID

90 75

CDNA

10;

41;

Length 208;

91

----LLGLSQLLQPEG 139

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A;Residues: 31-34,'X',36-43;48-51,'X',53-57;'X',60-71;159-164,'X',166-176;183-198,'X',20
A;Cross-references: UNIPARC:UPI0000176729; UNIPARC:UPI0000176728; UNIPARC:UPI000017672B;
G;Genetics: 14/1; 71/3; 107/3; 156/3
A;Introns: 14/1; 71/3; 107/3; 156/3
C;Superfamily: interleukin-6
C;Keywords: cytokine; growth factor; macrophage; monomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exodeoxyribonuclease V gamma chain XF0422 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa (cjate: 18-Mug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C;Accesion: A22809 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1121 < 65IM>
A; Residues: 1-1121 < 65IM>
A; Residues: 1-1121 < 65IM>
A; Cross-references: UNIPROT: Q9PG80; UNIPARC: UPI00000C23E1; GB: AE003893; GB: AE003849; NID
A; Experimental source: strain 9a5c
R; Simpson, A.J. G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
as-Neto, E.; Docena, C.; El-Dorry, H.; Fraga, J.S.; Franca, S.C.; Franco, D.M.; Carrer, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Marques, M. Martins, E.M.F.; Adsukuna, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak, A.Huthors: ad Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A.B.; A.B.; A.L.; A.B.; A.L.; A.B.; A.L.; A.B.; A.L.; A.L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 LLEQLCATYKLCHPEELVLLGH-----SLGIPKASL-SGCSSQALQQTQ--CLS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 QLHSGLCLYQGLL--QALSGISPALAPTLDLLQLDVANFATTIWQQMENLGVAPTVQP-- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 ETTNDVPHIQCGDGCDPQGLRDNSQPCLQRIHQGLIFYEKLLGSDIFTGE----PSLLP- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 LSQKLCTLAWSAHP----LVGHMDLREEGDEETTNDVPHIQCGDGCDPQGLRDNSQFCLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 VPGGSSPAWTQCQQLSQKL----CTL----AWSA----HPLVGHMDLREEGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342 PRLEDPSLOFHACHTRLRELOVLHDRLRALLEPNSPEGORFN----PPLOPRE 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- QPEGHHWETQQIPSLSPSQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 HHWETQQ-IPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVFAH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TQSAMPAFTSA--FQRRAGGVLAISYLQGFLETARLALHH 206
                                                                                                                                                                                                                                                                                                                    8.7%; Score 87.5; DB 2;
25.0%; Pred. No. 0.79;
tive 23; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 RIHQGLIFYEKLLGSDIFTG-EPSLLPDSPVAQLHAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
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Pred. No. 8;
18; Mismatches
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 41; Conserv
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Matches
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C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A24573
R;Nagata, S;. Tsuchiya, M.; Asano, S.; Kaziro, Y.; Yamazaki, T.; Yamamoto, O.; Hirata, Y. Nature 319, 415-418, 1986
A;Title: Molecular cloning and expression of cDNA for human granulocyte colony-stimulati
A;Reference number: A24573; MUID:86118679; PMID:3484805
A;Accession: A24573; MUID:86118679; PMID:3484805
A;Accession: A24573; MUID:86118679; PMID:3484805
A;Residues: 1-207 <MNA
A;Residues: 1-207 <MNA
A;Residues: L-207 <MNA
A;Residues: UNIPROT:P09919; UNIPARC:UPI0000128525; EMBL:X03438; NID:G31689; PIDR
C;Comment: This variant splice form is not expressed in three other cell lines and may r
C;Genetics:
C;Genetics:
A;Gene: GDB:CSF3
A;Cross-references: GDB:119083; OMIM:138970
A;Cross-references: GDB:119083; OMIM:138970
A;Cross-references: GDB:119083; OMIM:138970
A;Map position: 1741.2-17412
A;Introns: 14/1; 68/3; 104/3; 153/3
C;Superfamily: interleukin-6
C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer
F;1-30/Domain: signal sequence #status predicted <a href="Mill: 46077">MILLI CHU-2: #status
F;69-75,97-107/Product: granulocyte colony-stimulating factor variant splice form CHU-2: #status
F;69-75,97-107/Pisulfide bonds: #status predicted
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GAS6496
GAS66490
GAS666490
GAS6666490
GAS666490
GAS666400
GAS66400
GAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 -EPSILPDSPVAQIHASLIGISQLLQPEGHHWETQQIPSISPSQ------PWQRLLLR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GH------SLGIPWAPL-SSCALQ--LAGCLSQLHSGLFLYQGLL--QALEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WIVO-EATPLGPASSLPOSFLLKCLEOVRKIOGDGAALOEKLVSECATYKLCHPEELVLL
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25.5%; Pred. No. 0.64;
ive 20; Mismatches 76; Indels 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 WIAQGRAVPGGSSPAWTQ----CQQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 VLVASHLOSFLEVSYRVLRH 203
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A;Molecule type: protein
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Matches 51; Conserv
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A;Status: prelimina
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Length 1121;

26;

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us-10-797-157-2.rpr

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A,Cross-references: UNIPARC:UP10000029AF5; GB:J03783; NID:g198367; PIDN:AAA39301.1; PID: R;Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; S.Bodo, T., 2070-2073, 1988
A;Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6 A;Reference number: A60799; MUID:89062753; PMID:3264198
                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UP10000173673
R;Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
J. Exp. Med. 171, 965-970, 1990
A;Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a mon A;Reference number: $10241; MUID:90171860; PMID:2106569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: UNIPARC:UPI000016CB67; EMBL:XS1457; NID:g49738; PIDN:CAA35824.1; PIDN:RABAN, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; SImpson, R.J.
R.Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; SImpson, R.J.
B. E. J. Biochem. 217, 53-59, 1993
A,Title: Specific covalent modification of the tryptophan residues in murine interleukin A;Reference number: S38254; MUID:94039075; PMID:8223586
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule_type: protein
A;Residues: 38-60;75,'X',77-79;176-203 <ZHA>
A;Cross-references: UNIPARC:UP10000173674; UNIPARC:UP10000173675; UNIPARC:UP10000173676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; F;1-24/Domain: signal sequence #status predicted <SIG>F;25-211/Product: interleukin-6 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ģ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 FTGEPSLLPDSPVAQLHASLL--GLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKIL 166
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C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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22.9%; Pred. No. 1.4;
tive 20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 5
A;Introns: 7/1; 68/3; 106/3; 156/3
C;Superfamily: interleukin-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 22.9<sup>†</sup>
Matches 44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 KŠĽEEFLKÝTLŘ 206
                                                                                                                                                                                                                                                       A; Molecule type: protein A; Residues: 77-98 < SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-6 <BLA>
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                                                                                                                                                                                                                 A, Accession: A60799
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A/ACCESSION A27610
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A/ACCESSION A30571
A/ACCESSION A30
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A;Rebidues: 25-39, X', 41-42, X', 44-45 <VSN>
A;Rebidues: 25-39, X', 41-42, X', 44-45 <VSN>
A;Cross-recences: UNIPARC: UPIDO00173672
B;Chlu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
A;Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clon
A;Reference number: A40486; MUID:89017145; PMID:3262872
A;Accession: A40486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interleukin-6 precursor - mouse
N/Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatocy
                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: A30531; A27610; A30571; S01323; S12103; E34047; A26662; A40486; A60799; S1C
R;Tanabe, O.; Akira, S.; Kamiya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.
J. Immunol. 141, 3875-3881, 1988
A;Title: Genomic structure of the murine IL-6 gene. High degree conservation of potentia
                                                                                                                                                                                                                 acytoma growth factor
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A;Contents: tongue
A;Accession: JC7683
A;Molecule type: mRNA
A;Residues: 1-858 «KIT»
A;Cross-references: UNIPROT:Q91VA4; UNIPARC:UP100000230BB; DDBJ:AB049994
C;Comment: This protein, a seven-transmembrane receptor, serves as a mediator of the sic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myslomnocytic growth factor precursor - chicken
NyAlternate names: colony-stimulating factor cMGF
C;Species Gallub gallus (chicken)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42247; S03633
R;Sterneck, E.; Blattner, C.; Graf, T.; Leutz, A.
Mol. Cell. Biol. 12, 1728-1735, 1992
A;Title: Structure of the chicken myelomonocytic growth factor gene and specific activat A;Reference number: A42247; MUID:92195319; PMID:1549124
A;Accession: A42247
A;Stauus: preliminary
A;Molecule type: DNA
A;Residues: 1-201 .eSTE>
A;Residues: 1-201 .eSTE>
A;Residues: 1-201 .eSTE>
A;Cross-references: UNIPROT:P13854; UNIPARC:UPI000012F05A
A;Note: sequence extracted from NCBI backbone (NCBIN:89832, NCBIP:89836)
R;Leutz, A.; Damm, K.; Sterneck, E.; Kowenz, E.; Ness, S.; Frank, R.; Gausepohl, H.; Pa.
BMBO 1. 9, 175-181, 1989
A;Title: Molecular cloning of the chicken myelomonocytic growth factor (cMGP) reveals r.
A;Reference number: S03633; MUID:89231616; PMID:2785450
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XResidues: 1-201 <LEU-
A;Cross-references: UNIPARC:UP1000012F05A; EMBL:X14477; NID:g63596; PIDN:CAA32639.1; PI:
C;Superfamily: interleukin-6
R;Kitagawa, M.; Kusakabe, Y.; Miura, H.; Ninomiya, Y.; Hino, A.
Biochem. Biophya. Res. Commun. 283, 285-242, 2001
A;Title: Molecular genetic identification of a candidate receptor gene for sweet taste.
A;Reference number: UC7683; MUID:21222875; PMID:11322794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEP---SLLPDS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----DSPLVQASGG-----SQFCFGLICLGLFCLSVLL----FPGRPSSASCLAQQ 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVAQLHASLLG-LSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAAR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            643 PMA--HLPLTGCLSTLFLQAAETFVESELP-LS----WANWLCSY--LRGLWAWLVVLLA 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GSRAVMLLILLIPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEGDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           th 8.0%; Score 80; DB 2; Similarity 27.4%; Pred. No. 21; S1; Conservative 9; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.9%; Score 79.5; DE Best Local Similarity 28.6%; Pred. No. 4.3; Matches 36; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 4
C;Superfamily: metabotropic glutamate receptor
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | |- |: ||||
570 GEPUVLSLLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 51: Conserv
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Cipecies: Arabidopsis thaliana (mouse-ear cress)
Cipecies: Arabidopsis thaliana (mouse-ear cress)
Cipaces 102-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
CiAccession: D96810
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; anser, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: D96810
A;Accession: D96810
A;Accession: D96810
A;Accession: D96810
A;Accession: D96810
A;Cross-references: UNIPROT:Q9C980; UNIPARC:UPI00000445D0; GB:AE005173; NID:g6587860; PI
C;Genetics:
A;Genetics:
A;Map position: 1
                                               A;Cross-references: UNIPROT:O06567; UNIPARC:UPI0000D0F2A; GB:295585; GB:AL123456; NID:g
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv1115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---PSLLPDSPVAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQ--- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 HMYLPMDVDAGEDQPPA--PDEPVTAVDD-----VEPE-------MPAPCPTQRPP 177
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: JC7683
                                                                                                                                                                                                                                                                                                                                                                                       9 LILLILPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEGDEE----
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LLEASD---ACEEALRINPT--YERAHQR---LASLQLRLGEVEKALCH 249
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                                                                                                                                                                                                                                                    2; Length 232;
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Best Local Similarity 25.7%; Pred. No. 11;
Matches 28; Conservative 22; Mismatches 38;
                                                                                                                                                                                                                                            Query Match 8.0%; Score 80.5; DB Best Local Similarity 23.4%; Pred. No. 4.1; Matches 49; Conservative 27; Mismatches
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. Yuan, Z.; Liu, W.; Hammes, G.G.
C.C. Natl. Acad. Sci. U.S.A. 85.
Title: Wolecular cloning and sequencing of DNA complementary to chicken liver fatty ac
Reference number: A31236, MUID:88320436, PMID:2842766
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Ay Residues: 1752-2512 < YUA2>

Ay Residue: 1752-2512 < YUA2>

Ay Residue: 1752-1757 | Pazirandeh, M.; Stolow, D.T.; Huang, W.Y.; Wakil, S.J.

Biol. (Chem. 264, 3750-3757, 1989

Ay Title: A novel CDNA extension procedure. Isolation of chicken fatty acid synthase CDNA

Ay Reference number: A30297; MUID:89139426; PMID:2917973
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A;Residues: 1568-2512 <CHI>
A;Cross-references: UNIPARC:UP100001723E3; EMBL:J04485; NID:g460908
A;Cross-references: UNIPARC:UP100001723E3; EMBL:J04485; NID:g460908
A;Nore: neither the complete nucleic acid sequence nor the complete translation are show:
R;Yang, C:Y:; Huang, W:Y:; Chirala, S.; Wakil, S.J.
Biochemistry 27, 7773-7777, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Characterization of a genomic and cDNA clone coding for the thioesterase domain A; Reference number: A31185; MUID:89088152; PMID:3207710
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A;Residues: 2202-2512 <KAS1>
A;Cross-references: UNIPARC:UPI00001723E5; EMBL:J02839; NID:g211768; PIDN:AAA82106.1; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein

A; Residues: 144-166;575-583;2141-2165 < CHA1>
A; Residues: 144-166;575-583;2141-2165 < CHA1>
A; Cross-references: UNIPARC: UP100001723DB, UNIPARC: UP100001723DC; UNIPARC: UP100001723DD

B; Holzer, K.P.; Liu, W.; Hammes, G.G.

B; Holzer, K.P.; Liu, W.; Hammes, G.G.

A; Holzer, K.P.; Liu, M.; Hammes, G.G.

A; Hitle: Molecular cloning and sequencing of Chicken liver fatty acid synthase cDNA.

A; Reference number: A33918; MUID: 89282777; PMID: 2734291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Title: Complete amino acid sequence of the thioesterase domain of chicken liver fatty A,Reference number: A31184; MUID:89088151; PMID:3207709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;MOlecule type: mRNA
A;Residues: 75-77,'PV',80-116,'A',118-675,'S',677-1169,'N',1171-1178,'T',1180-1191,'H'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Amino acid sequences of substrate-binding sites in chicken liver fatty acid A;Reference number: A29967; MUID:89000676; PMID:3167014
A;Accession: A29967
                                                                                             the animal fatty acid
                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-182 <HUA2>
A;Cross-references: UNIPARC:UPI00001723D9; EMBL:J04485; NID:g460908
R; Huang, W.Y.; Chirala, S.S.; Wakil, S.J.
Arch. Biochem. Biophys. 314, 45-49, 1994
A;Title: Amino-terminal blocking group and sequence of t
A;Reference number: S51519; MUID:95031085; PMID:7944406
A;Accession: S51519
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A;Residues: 2209-2508 < YAN>
A;Residues: 2209-2508 < YAN>
A;Cross-references: UNIPARC:UPI00001723E4
R;Kasturi, R.; Chirala, S.; Pazirandeh, M.; Wakil, S.J.
Biochemistry 27, 7778-7785, 1988
A;Title: Characterization of a genomic and cDNA clone of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ./Molecule type: mRNA
/,Residues: 1752-2350, 'CFSFSLFQ', 2351-2512 <YUAl>
/,Crossles-references: UNIPARC:UPI00001723E1
/,Accession: B31236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: determination of acetylated amino end
                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 1-12 <HUA3>
A;Crose-references: UNIPARC:UPI00001723DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 107-113;1086-1091 <HOL1>
A; Cross-references: UNIPARC: UP100001723DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPARC:UPI00001723DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chang, S.I.; Hammes, G.G.
                                                                                                                                                                                                                                                                                                                                                         A; Accession: A30620
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Cypecies: Gallus gallus (chicken)
Cypecies: Gallus gallus (chicken)
Cypecies: Gallus gallus (chicken)
Cypecies: Jo-Sep-1991 #sequence revision 12-Apr-1996 #text_change 09-Jul-2004
CyAccession: 557248; S51519; A30620; A29967; A33918; A30445; A31236; B31236; A30297; A31
RyHuang, W.Y.; Chirala, S.S.; Wakil, S.J.
RyBecription: Amino-terminal blocking group and sequence of the animal fatty acid synth Axecession: 557248
AyAccession: 557248
AyAccession: 557248
AyAccession: 257248
AyAccession: Laberty (Company 1989)
AyAccession: 257248
AyAcce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UPI000005A4B3; GB:AL513382; PIDN:CAD07741.1; PID:g16504293; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                          HNLVRHPDMPKAAFADMWYTLKQGEPWSGIVKNRRKNGDHYWVRANAVPMIREGRVTGYM 112
        --NSQFCLORIHOGLIFYEKLLGSDIFTGEPSLLPDSPVAQ 123
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C;Superfamily: methyl-accepting chemotaxis protein
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; Pred. No. 14;
19; Mismatches
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R; Huang, W.Y.; Stoops, J.K.; Wakil, S.J.

Arch. Biochem. Biochem. Biophys. 270, 92-98, 1989

A; Title: Complete amino acid sequence of chicken liver acyl carrier protein derived from A; Reference number: S03856; MUID:89192401; PMID:2648999

A; Accession: S03856

A; Molecule type: protein

A; Residues: 2121-2209 (HUA4>

A; Cross-references: UNIPARC:UPI0000172356

A; Cross-references: UNIPARC:UPI000017236

A; Cross-references: UNIPARC:UPI000017236

A; Residues: 23-3789. 1989

A; Title: Amino acid sequences of pyridoxal 5'-phosphate binding sites and fluorescence IA; Reference number: A32015; MUID:89323081; PMID:2751995

A; Residues: 667-675; L699-1709 (CHA2>

A; Residues: 667-675; L699-1709 (CHA2>

A; Cross-references: UNIPARC:UPI00001723E8

A; Note: the binding of pyridoxal 5'-phosphate to Lys-1708 competitively inhibits the bin C; Function: cHPD>

A; Description: as 3-hydroxypalmitcyl-[acyl-carrier-protein] debydratase (EC 4.2.1.61) ca
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Pathway: fatty acid biosynthesis

C;Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I home

C;Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase; a

C;Superfamily: abort-chiain alcohol dehydrogenase homology; dacyl-carrier-protein] S-

C;Reywords: acetylated amino end; acyl-transferase; alternative splicing; carbon-oxygen ]

P; oxidoreductase; phosphopantetheine; phosphoprotein; thiolester hydrolase

F;1-2512/Product: fatty-acid synthase; splice form 1 #status predict

F;1-2350, CFSFELFQ; 2351-2512/Product: fatty-acid synthase I homology <0ASH>

F;22-404/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <0ASH>

F;32-1340/Region: caralytic (of 3-hydroxypalmitcyl-lacyl-carrier-protein] dehydratase)

F;1554-1858/Domain: long-chain alcohol dehydrogenase homology <ADH>

F;155-109/Domain: acyl-carrier protein homology <ACP>

F;2133-2193/Domain: acyl-carrier protein homology <ACP>

F;2133-2193/Domain: acyl-carrier protein homology <ACP>

F;214-2487/Domain: oleoyl-carrier-protein] hydrolase homology <ACP+
A;Molecule type: mRNA k;AsS2> k;Residues: 2202-2512 k;RAS2> k;Residues: 2202-2512 k;RAS2> k;Residues: 2202-2512 k;RAS2> k;Residues: 2202-2512 k;RAS2> k;Residues: 202-2512 k;RAS2> k;RAS3-2517 k;RAS3-
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DB 1; Length 2512;

7.9%; Score 79;

Query Match

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hypothetical protein F6H11.10 - Arabidopsis thaliana (5Species: Arabidopsis thaliana (mouse-ear cress) (5Species: Arabidopsis thaliana (mouse-ear cress) (5.Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Jul-2004 (5.Accession: T05882 (7.Accession: T05882 (7.Accession: P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Bancroft, I.; Mewreubmitted to the Protein Sequence Database, April 1998 (7.Accesion: 215456 (7.Accesion: A)Reference number: 215456
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                                                                                                                                                         1170 KGAAAGSPPAQKGLQHILTEICRLELNGNP---HSEL----EQIVTQEKMHLQ----DDP
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A;Molecule type: DNA
A;Residues: 1-1026 - 6EBV>
A;Cross-references: UNIPROT:O49529; UNIPARC:UPI0000A2380; EMBL:AL021684
A;Experimental source: cultivar Columbia; BAC clone F6H11
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cive 18; Mismatches 5:
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A;Introns: 37/2; 109/1; 115/2; 560/1; 737/1; 833/3
A;Note: F6H11.10
Best Local Similarity 23.3%; Pred. No. 93; Matches 37; Conservative 23; Mismatches
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Q2n2p6 aeromonas h
Q3hi79 trichodesmi
O9pg80 xyleila fas
O9pz44 multipla ac
O9nrz4 homo sapien
Q75138 oryza sativ
Q3u8j8 mus musculu
Q3u655 mus musculu
Q6865 homo sapien
Q7z3m6 homo sapien
Q7z3m6 homo sapien
Q3rsz xylella fas
              Q3HI79_TRIER
Q9PG80_XYLFA
Q9PZ44_9RETR
GAW2_HUMAN
Q75138_MOUSE
IL6_MOUSE
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Q68D85
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ALIGNMENTS

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61 DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUCLEOTIDE SEQUENCE.
MEDLINE=20567322; PubMed=11114383; DOI=10.1016/S1074-7613(00)00070-4; Oppmann B., Lesley R., Blom B., Timans J.C., Xu Y., Hunte B., Vega F., Yu N., Wang J., Singh K., Zonin F., Vaisberg E., Churakova T., Liu M.-R., Gorman D., Wagner J., Zurawski S., Liu Y.-J., Abrams J.S., Moore K.W., Rennick D., de Waal-Malefyt R., Hannum C., Bazan J.F., Kastelein R.A.;
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20744 MW; BFB5C0F42D4C1E3A CRC64;
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Ensembl; ENSG0000110944; Homo sapiens.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR012351; Cytokine 4 hlx.
InterPro; IPR012351; ILE MGF GCSF.
PANTHER, PTHR15947; ILE3A.
                                                                                                    01-MAR-2001, integrated into UniProtKB/TrEMBL.
01-MAR-2001, sequence version 1.
07-FEB-2006, entry version 16.
Interleukin 23 p19 subunit.
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Q9H2AS HUMAN PRELIMINARY; PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLECTIDE SEQUENCE.

NUCLECTIDE SEQUENCE.

TISSUB-PCR rescued clones;

X Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Straubberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Straubberg R.P., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Stableton M., Moore T., Max S.I., Wang J., Haidh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,

Brownstein M.J., Uddin T.B., Toohlyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunsarene P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,

Blakebley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Warra M.A.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Warra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUCLEOTIDE SEQUENCE.

RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,

Chen J., Chow B., Chui C., Crowley C., Currell B., Douel B., Dowd P.,

RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

RA Lewis E., Nark M.R., S., Kimwowski L., Johnson S., Lee J.,

RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandlen R.L., Matanabe C., Wieand D., Woods K., Xie M.-H.,

Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,

RA Wood W.I., Godowski P.J., Gray A.M.;

RT secreted protein discovery initiative (SPDI), a large-scale

Fifort to identify novel human secreted and transmembrane proteins: a

RI Genome Res. 13:2265-2270(2003).
Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                01-OCT-2000, integrated into UniProtKB/TrEMBL.
01-CCT-2000, sequence version 1.
01-CEB-2006, entry version 22.
SGRF precursor (IL-23 p19) (Interleukin 23, alpha subunit p19,).
Names-SGRF; SynonymasTL23A; ORFNames-UNQ2498;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Spleen;
Hirata Y., Kosuga Y.;
"SORF; a novel member of the IL-6/G-CSF family.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Director MGC Project;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                    189 AA
                                                                                                                                                                    PRT;
                                                                                                                                                                   Q9NPF7_HUMAN PRELIMINARY;
Q9NPF7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
TISSUE=PCR rescued clones;
                                                   AHGAATLSP 189
                                                                                    181 AHGAATLSP 189
                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubserg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
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                                                                                                             Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 19 Potential.
20 189 SGRF.
189 AA; 20730 MW; 51B5C0F188EC1B9F CRC64;
                                                                                                                                                                                                                                                      EMBL; AB030000; BAA93686.1; -; mRNA.

EMBL; AY359083; AA069442.1; -; mRNA.

EMBL; BC066258, AA466268.1; -; mRNA.

EMBL; BC067511; AA467511.1; -; mRNA.

EMBL; BC067512; AA467512.1; -; mRNA.

EMBL; BC067513; AA467513.1; -; Genomic_DNA.

ENSEMD; BC06000110944; Homo saplens.

GO; GO:0005157; F:CYtokine activity: IEA.

GO; GO:0005157; F:CYtokine activity: IEA.

GO; GO:0005157; F:CYtokine 4_hlx.

InterPro; IPR012351; Cytokine 4_hlx.

InterPro; IPR01351; IL23A.

InterPro; IPR003573; IL6_MGF_GCSF.

PANTHER; PTHR15947; IL23A; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 AA.
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SGRF.
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QGNZ827
[5]
NUCLEOTIDE SEQUENCE.
TISSUE=PCR rescued clones;
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                                                                                        Strausberg
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Pilalon D.K., Muzuy D.W., Sodergren B.J., Lu X., Gibbs R.A.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,
A Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DEETINDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSF 120
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Best Local Similarity 98.4%; Pred. No. 1.9e-83;
Matches 186; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Director MGC Project;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, BC066267; AAH66267.1; -; mRNA.

Bnsembl, ENSG0000110944; Homo sapiens.
GO; GO:0005276; C:extracellular region, IEA.
GO; GO:0005125; F:extracellular region, IEA.
GO; GO:0005125; F:extracellular region, IEA.
InterPro; IPR013351; Cytokine 4 hlx.
InterPro; IPR010931; IL23A.
InterPro; IPR010931; IL23A.
InterPro; IPR03573; IL6 MGF GCSF.
PANTHER; PTHR15947; IL23A; I.
PFam; PF00489; IL6; 1.
Pfam; PF00489; IL6; 1.
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Q6NZ80;
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TISSUE=PCR rescued clones;
                                                                                                                                                                                                                                                                                                                                                       cDNA sequences.
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NCBI_TaxID=9606;
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HUMAN
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NUCLECTIDE SEQUENCE.

TISSUB-PCR rescued clones;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A trausberg R.D., Feingold B.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B. Buetow K.H., Schemen C.M., Schuler G.D.,

A thachal S.F., Zeeberg B. B. Buetow K.H., Schaefer C.F., Bhard N.K.,

Hopkins R.F., Jordan H., Moore T., Max J.L., Wang J., Haish F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Boosk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Natchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield M., Schein J.E., Jones S.J.M., Marra M.A.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

"""" "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Pred. No. 5.4e-83;
Pred. ----Ahas 2; Indels
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GO; GO:0005576; C:extracellular region; IBA.

GO; GO:0005125; F:cytokine activity; IEA.

GO; GO:0005125; F:cytokine activity; IEA.

INTERPRO; IPR012351; Cytokine 4 hlx.

INTERPRO; IPR01351; IL23A.

INTERPRO; IPR03573; IL6 MGF GCSF.

PANTHER; PFHR15947; IL23A; I.

SEQUENCE 189 AA; 20718 MW; 594290F188EC1B9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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98.9%; Pred. No. 5...
... 0; Mismatches
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Ensembl; ENSG0000110944; Homo sapiens.
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TISSUE=PCR rescued clones;
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Matches 186; Conservative
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 EEGDEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLP 117
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Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                            Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Laurasiatheria, Perissodactyla, Equidae, Equus. (CDI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3,
                                                                                                                                                                                                                                            PubMed=16293125;
Musllova P., Kubickova S., Vychodilova-Krenkova L., Kralik P.,
Matiasovic J., Hubertova D., Rubes J., Horin P.;
"Cytogenetic mapping of immunity-related genes in the domestic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AY704416; AAU33947.1; -; Genomic DNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR012351; Cytokine 4_hlx.
InterPro; IPR012351; Cytokine 4_hlx.
InterPro; IPR012351; IL23A.
InterPro; IPR01831; IL23A.
PANTHER; PTHR15947; IL23Ā; 1.
PEAM; PF00489; IL6; 1.
SEQUENCE 192 AA; 21042 MW; 9898C79BC9E22E4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 873.5; DB 2
Pred. No. 2.5e-72;
8; Mismatches 12
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Interleukin 23 p19 subunit.
Equus caballus (Horse).
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Matches 169;
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REEGDEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 REEGDDETTSEVPHIQCGDGCDPQGLRDNSQSCLQRIHQGLVFYEKLLGSDIFTGEPSLH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 PDSPVAQLHASILGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVA 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MICSRAVMIMILILILIPWTSQGRAVPEGSSPAWAQGQUISQQLCTLAWTAHLPMGHVDLP
                                                                                                                                                                                                                                                                                                                                                                                                                           1 MIGSRAVM---LLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMD-LREE
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05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 8.
Interleukin-23 pl9 subunit.
Name-IL-23 pl9 subunit.
Cavia porcellus (Guinea pig).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
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                                                                                                                                                                                                                                                                                       Query Match
84.3%; Score 846; DB 2; Length 193;
Best Local Similarity 85.4%; Pred. No. 8.8e-70;
Matches 164; Conservative 10; Mismatches 14; Indels
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GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0005125; P:immune response; IEA.
Interpro; IPR012351; Cytokine_4_hlx.
Interpro; IPR012351; Cytokine_4_hlx.
Interpro; IPR01351; IL23A.
Interpro; IPR03573; IL6 MGF GCSF.
PANTHER; PTHR15947; IL23Ā; I.
PĒAM; PP00489; IL6; 1.
SEQUENCE 189 AA; 20808 MW; BE06A3C59955337F CRC64;
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                         InterPro; IPR012351; Cytokine 4 hix.
InterPro; IPR010831; IL23A.
InterPro; IPR03573; IL6 MGF GCSF.
PANTHER; PTWAT15947; IL23A; 1.
PFam; PF00489; IL6; 1.
SEQUENCE 193 AA; 21132 MW; 05F28DE94810B9E1 CRC64;
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GO; GO:0005125; F:cytokine activity; GO; GO:0006955; P:immune response; Il
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MEDLINE-2238625; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschnko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M.J., Goares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robask S.A., McEwan P.J., McKernan K.J., Malek J.A., Hulyk S.W.,

Robask S.W., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Loquellano N.A., Sodergren E.J., Lu X., Gibbs R.A.,

Robask S., Worley K.C., Hale S., Garcia A.M., Robrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rotriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                  Tran G., Hodgkinson S.;
"Rattus norvegicus IL-23 mRNA.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH MGC Project;
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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EMBL, BCO98907; AAH98907.1; -; mRNA.
Ensembl, BNSRNGG00000003254; Rattus norvegicus.
RGD, G20873; I123a.
GO; GO:0005125; F:Cyrokinin activity; IEA.
GO; GO:0005125; F:Cyrokinin activity; IEA.
GO; GO:0006955; P:Ammune response; IEA.
InterPro; IPR012351; Cyrokine_4_hlx.
InterPro; IPR012351; Cyrokine_4_hlx.
InterPro; IPR012373; IL6 MGF GCSF.
PANTHER; PTHR15947; IL23Ā, 1.
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                                                                        NUCLEOTIDE SEQUENCE
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NCBI_TaxID=10116;
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                                                                        61 DLPREGGDD5TTDDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLVFYEKLLGSBIFTGSP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                 120 PVAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARV
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea, Muridae; Murinae, Rattus.
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07-FBB-2006, entry version 2.
Interleukin 23 pl9 subunit (Fragment).
Elis silvestris catus (Cat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae; NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
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79.6%; Score 799.5; DB 2; Length 185;
Best Local Similarity 82.7%; Pred. No. 1.66-65;
Matches 153; Conservative 10; Mismatches 15; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peters I.R., Waly N.;
Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
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185 AA, 20433 MW, 344A2940AAFB773B CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QZQS96 FELCA PRELIMINARY; PRT; 185 AA. Q2QS86; 24-JAN-2006, integrated into UniProtKB/TrEMBL.
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01-DEC-2001, sequence version 1.
07-FEB-2006, entry version 14.
Interleukin 23, alpha subunit p19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; DQ195102; ABB01676.1; -; mRNA.
NON TER 185 185
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180 FAHGAATLS 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DESTINDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLFYEKLLGSDIFIGEPSLLPDSP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DEEPRNDVPRIQCGDGCDPQGLKDNSQFCLQRIHQGLVFYKQLLDSDIFTGEPSLLPDDP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVF 180
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                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution.NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MIGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MLDCRAILLLWLLPWTAQGLAVPRTSSPDWAQCQQLSRNLCTLAWSAHPPVGHTDTLREE
                                                                                                       Peromyscus maniculatus (Deer mouse).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Cricetidae; Neotominae; Peromyscus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muns musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 NOUSE
09EQ14 WOUSE PRELIMINARY; PRT; 196 AA.
09EQ14 WOUSE PRELIMINARY; PRT; 196 AA.
01-MAR-2001, integrated into UniProtKB/TrEMBL.
01-MAR-2001, sequence version 1.
07-FEB-2006, entry version 21.
Interleukin 23 p19 subunit (Interleukin 23, alpha subunit p19).
                                                                                                                                                                                                                                                                                                                                                                                                      76.5%; Score 768; DB 2; Length 184; 78.7%; Pred. No. 1.3e-62; Ive 11; Mismatches 28; Indels
                                                                                                                                                                                      Schountz T.; "Cloning of deer mouse interleukin-23a p19 subunit."; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                184 AA; 20850 MW; 4045456CF6ACA1C8 CRC64;
                                                                                                                                                                                                                                                                EMBL; AY259629; AAP15041.1; -; mRNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005125; F:cyrokine activity; IEA.
GO; GO:0006955; P:cyrokine activity; IEA.
InterPro; IPR012351; Cytokine 4_hlx.
InterPro; IPR01031; IL23A.
InterPro; IPR003573; IL6_MGF_GCSF.
PANTHER; PTHR19947; IL23A; 1.
Pfam; PF00489; IL6; 1.
                                                          01-0707-2003, integrated into UniProtKB/TrEMBL 01-07UN-2003, sequence version 1. 07-FEB-2006, entry version 7. Interleukin-23a subunit p19 (Fragment).
                                          184 AA
                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 78.78 Matches 144; Conservative
                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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                                      QBOWE2 PERMA F
QBOWE2;
01-JUN-2003, int
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NUCLECOTIDE SEQUENCE.

STRAIN=FUB/N; TISSUB-Mammary tumor. C3;

NUCLEDINE=2238825; PubMed=12477932; DoI=10.1073/pnas.242603899;

Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Altachul S.F., Zeeberg B., Buerow K.H., Schamen C.M., Schuler G.D.,

Altachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heideh F.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Astapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
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MEDLINB=20567322; PubMed=11114383; DOI=10.1016/S1074-7613(00)00070-4; Oppmann B., Lesley R., Blom B., Timans J.C., Xu Y., Hunte B., Vega F., Yu N., Wang J., Singh K., Zonin F., Vaisberg E., Churakova T., Liu M.-R., Gorman D., Wagner J., Zurawski S., Liu Y.-J., Abrams J.S., Moore K.W., Rennick D., de Waal-Malefyt R., Hannum C., Bazan J.F.,
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                                                                                                                                                                                                                                                            "Novel p19 procein engages IL-12p40 to form a cytokine, IL-23, with biological activities similar as well as distinct from IL-12."; Immunity 13:715-725(2000).
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SEQUENCE 196 AA; 22071 MW; DAF4A318A2DD3B7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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71.6%; Score 718.5; DB 2;
Best Local Similarity 74.6%; Pred. No. 5.3e-58;
Matches 141; Conservative 14; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AF301619; AAG37231.1; -; mRNA.
EMBL, BC019953; AAH1953.1; -; mRNA.
Ensembl, BNSW18000000025383; Mus musculus.
MG1; MG1:1932410; 1123a.
GO; GO:0005615; C:extracellular space; RCA.
InterPro; IPR010351; Cytokine_4 hlx.
InterPro; IPR010351; LU23A.
InterPro; IPR003573; ILG_MGF_GCSF.
InterPro; IRR003573; ILG_MGF_GCSF.
PANTHER; PTHR1547; ILG23A; 1.
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STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
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Query Match
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ENBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suldae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- PQNLVGRF-AELWGWMEQELKPNGVFALHWDEFTGDDDFKDLPPVKPWQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 LLPDSPVAQLHASLLG-LSQLLQPEG---HHWB----TQQIPSLSPSQPWQ 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.7%; Score 107; DB 2; Length 236; 28.8%; Pred. No. 0.19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 236 AA; 28574 MW; 84011B98C36AC47C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                002837; 019180;
15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
30-MAY-2000, sequence version 2.
07-FEB-2006, entry version 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AAFB01000228; EAL48883.1; -; Genomic_DNA.
                                                                                                                                                                               07-JUN-2005, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=15729342; DOI=10.1038/nature03291;
                                                                                                                                                                                                                                                                                       Entamoeba histolytica HM-1:IMSS.
Eukaryota, Entamoebidae, Entamoeba.
NCBI_TaxID=294381,
                                                                                                                                      PRT;
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                                                                                                                                                                                                    07-JUN-2005, sequence version 1.
07-FEB-2006, entry version 3.
Hypothetical protein.
                                                                                                                                      PRELIMINARY;
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NUCLEOTIDE SEQUENCE [MRNA]
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181 FAHGAATLT 189
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                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                     ORFNames=58.t00019;
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                                                                                                                                   Q516V9 ENTHI
Q516V9;
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Matches
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47 AHP----LVGHMDLREEGDEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 CHPQELVLLGH-----SLGLPQASL-SSCSSQALQLTG--CLNQLHGGLVLYQG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 LLGSDIFTG-EPSLLPDSPVAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQ----- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----QLSQKLCTLAWS 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                      TISSUE-LIVET, Sandeman R.M., Strom A.D.G.;
Gloster S.E., Sandeman R.M., Strom A.D.G.;
"Cloning of a cDNA and gene encoding porcine granulocyte-colony
stimulating factor.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: Granulocyte/macrophage colony-stimulating factors are
cytokines that act in hematopoiesis by controlling the production,
differentiation, and function of 2 related white cell populations
of the blood, the granulocytes and the monocytes-macrophages. This
CSF induces granulocytes (By similarity).
-!- SUBGNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LMALQLLLWHIALWMVPEAAPLSPASSLPQSFLLKCLEQVRKIQADGAELQERLCATHKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
MEDLINE=97473512; PubMed=9332386; DOI=10.1016/S0378-1119(97)00284-9; Kulhdurg P., Radke M., Mezes B., Mertelsmann R., Rosenthal F.M.; e.Cloning and sequence analysis of the immediate promoter region and cDNA of porcine granulocyte colony-stimulating factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Granulocyte colony-stimulating factor. /FTid=PRO 0000015572.
O-linked TGalNAc. . .) (By similarity). By similarity. By similarity. A -> R (in Ref. 1). MW, 84787F20DB0AEAIC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.6%; Score 106.5; 'DB 1; Length 195; 24.9%; Pred. No. 0.17; tive 28; Mismatches 76; Indels 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBUNIT: Monomer.
-1- SUBCELLULAR LOCATION: Secreted protein.
-1- FIF: 0-19/2008/lated (By similarity).
-1- SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The factor; Signal. Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 VMLLLLLPWTAQGRAVPGGS--SPAWTQCQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 -PWORLLLRFKILRSLQAFVAVAARVFAH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | | : : | | : : | | : 191
163 SAFQRRAGGVLVVSQLQSFLELAYRVLRY 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Y10494; CAA71518.1; -; mRNA.
EMBL; U66482; AAB70701.1; -; Genomic_DNA.
EMBL; U68481; AB570700.1; -; mRNA.
HSSP; P09919; 1RHG.
SWR; O02837; 26-195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200
                                                                                                                                                                  NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR012351; Cytokine 4 hlx.
InterPro; IPR003629; GCSF MGF.
InterPro; IPR003573; IL6_MGF_GCSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00254; INTERLEUKIN 6; 1. Cytokine; Glycoprotein; Growth fact. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00433; ILGGCSFMGF.
ProDom; PD008388; GCSF MGF; 1.
SWART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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63
95
123
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                                                                                                               Gene 197:361-365(1997)
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57
85
123
195 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBN4W3 HUMAN
QBN4W3;
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DISULFID
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67 LCHPEBLVLLGH-----SLGIPWAPL-SSCPSQALQ--LAGCLSQLHSGLFLYQ 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0433; ILGGCSFMGF.
PRINTS; PR00434; INTERLEUKING.
SMART; SM00126; ILG; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR012381; Cytokine 4 hix
InterPro; IPR003573; IL6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
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                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 25.9% tes 51; Conservative
                                                                                                                                                                                                                                                                                 07-FEB-2006, entry vers
CSF3 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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SEQUENCE
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                                                                                                                                                                                    MEDINE-228825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDINE-228825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E., Brapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Araba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anthing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anthing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anthing M., Mathan J.W., Schheit J. Skalksa U., Smailus D.B., Butterfield Y.S.N., Krzywinski M.I., Skalksa U., Smailus D.B., M.A., Schherch A., Schein J.B., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 SAHP----LVGHMDLREEGDEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 SRAVMILL--LIPWTAQGRAVPGGSSPAWTQ----CQQ------LSQKLCTLAW 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JUN-2002) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO: 0005615; C: extracellular space; IEA.
GO; GO: 0005125; F: cytokine activity; IEA.
GO; GO: 0005135; F: cytokine activity; IEA.
GO; GO: 000555; P: cytokine activity; IEA.
InterPro; IPR012351; Cytokine 4 hlx.
InterPro; IPR003529; GCSF MGF.
InterPro; IPR003579; ILG MGF GCSF.
InterPro; IPR003574; Interleukin 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00254; INTERLEUKIN 6; 1.
SEQUENCE 200 AA; 21543 MW; 8648AA55B329A96C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
   01-OCT-2002, integrated into UniProtKB/TrEMBL. 01-OCT-2002, sequence version 1. 21-FEB-2006, entry version 20. Colony stimulating factor 3, isoform c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.2%; Score 102; DB 2
26.7%; Pred. No. 0.45;
ive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P09919; 1GNC.
SMR; QBN4W3; 30-200.
Ensembl; ENSG0000108342; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC033245; AAH33245.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD008388; GCSF MGF; 1.
ProDom; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00433; ILGGCSFMGF.
PRINTS; PR00434; INTERLEUKING.
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                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rissue-skin;
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                                                               113 GLL--QALEGISPELGPTLDTLQLDVADFATTIWQQME----ELGMAPALQPTQGAMPAF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 DLREEGDEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTG-EP 113
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102 KLLGSDIFTG-EPSLLPDSPVAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQ----- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 WTVQ-EATPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGH- 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 WTAQGRAVPGGSSPAWTQ----CQQ-----LSQKLCTLAWSAHP----LVGHM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S., Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W., Korn B., Zuo D., Hu Y., LaBaer J.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21978 MW; 5F07C52F13D6A6D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ensembl; NSG00000108342; Homo sapiens.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005128; F:cytokine activity; IEA.
GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2005, integrated into UniProtKB/TrEMBL. 10-MAY-2005, sequence version 1. 07-FEB-2006, entry version 3.
                                                                                                                                                                                         -- PWORLLLRFKILRSLQAFVAVAARVFAH 182
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Search completed: June 20, 2006, 04:39:26 Job time : 215.627 secs

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Query Match 100.
Best Local Similarity 100.
Matches 189; Conservative
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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; MOLECULE TY
US-09-122-443-2
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/EMC_Celerra_SIDS3/ptodata/2/laa/7_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/laa/H_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/laa/PCTUS_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/laa/PCTUS_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/laa/RE_COMB.pep:*
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Maximum Match 100%
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1002		RESULT 1 US-09-122-443-2 Sequence 2, Application US/ Sequence 2, Application US/ Berent No. 6060284 GENERAL INPORMATION: MAM NUMBER OF ENUENTION: MAM NUMBER OF ENUENTION: MAM NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS: ADDRESSEE: DNAX Resea STREET: 901 California CITY: Palo Alto STATE: California COUNTRY: USA ZIP: 94304-1104 COMPUTER: EBM PC COMPORTER: IBM PC COMPORTER: ASE COMPORTER: CALCUL-1 FILING DATE: 25-UJL-1 FILING DATE: 25-UJL-1 FILING DATE: 25-UJL-1 FILING DATE: 25-UJL-1 FILING DATE: CALCUL-1 FILING DATE: CALCU
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Length 189; Indels

Score 1004; DB 2; Pred. No. 1.6e-106; ; Mismatches 0;

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TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
STREET: 901 California Avenue
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US 60/053,765
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/558,087
FILING DATE: 25-Apr-2000
CLASSIFICATION: «Unknown»
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                            Sequence 2, Application US/09558087; Patent No. 6495667; GENERAL INFORMATION:
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US-09-558-474-2
'Sequence 2, Application US/09558474
'Patent No. 6835825
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TYPE: amino acid
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STATE: California
COUNTRY: USA
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                                               61 DEETINDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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Patent No. 6479634
GENERAL INFORMATION
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/558,089
FILING DATE: 25-Apr-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION OF AURHOWN»
APPLICATION NUMBER: 09/122,443
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ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-558-089-2
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SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 189; Conservative
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Query Match 100.
Best Local Similarity 100.
Matches 189; Conservative
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CORGANISM: Homo sapiens
US-09-687-637B-1
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Patent No. RE39015
GENERAL INFORMATION
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: DARA Research Institute
STREET: 901 California Avenue
                 APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INDEP Compatible
COMPUTER: INDEP Compatible
CONFURER: INDEP Compatible
CORFATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/558,474
FILING DATE: 25-Apr-2000
CLASSIFTCATION: dinknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/053,765
FILING DATE: 25-JUL-1997
ATTORNEY/AGNT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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100.0%; Score 1004; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.6e-106;
Matches 189; Conservative 0; Mismatches 0;
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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(650)496-1200
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TYPE: amino acid
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SEQUENCE CHARACTERISTICS
                                                                                                                                                           CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AHGAATLSP 189
                                                                                                                                                                                                       COUNTRY: USA
GENERAL INFORMATION:
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PVAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARV 179
                                                       61 EDEETKONVPRIQCEDGCDPQGLKDNSQFCLQRIRQGLAFYKHLLDSDIFKGEPALLPDS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 GDEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLDCRAVIMEMELEPWYTQGLAVPRSSPDWAQCQQLSRNLCMLAWNAHAPAGHMNLLREE
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                                                                                                                                                                                                               Length 196;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 196 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELEFAX: (650) 496-1200
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                                                                                                       180 FAHGAATLS 188
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                                                                                                                                        61 DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
                                                                                                                                                             61 DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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                                                                                                                                                                                                            VAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRPKILRSLQAFVAVAARVF 180
                                                                                                      1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG 60
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                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 4 Application US/09122443; Patent No. 6060284; Patent No. 6060284; Patent No. 6060284; Throw Manager Sequence Title OF Invervion: Manager Sequences: 16; CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESSE: DATA Research Institute STREET: 901 California Avenue CITY: Palo Alto COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 196;
     Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Score 718.5; DB 2; Length 1
, Pred. No. 7.3e-74;
14; Mismatches 33; Indels
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/122,443 FILING DATE: 24-JUL-1998 CLASSIFICATION DATA: PAPLICATION DATA: PAPLICATION DATE: PAPLICATION DATA: APPLICATION NUMBER: US 60/053,765 FILING DATE: 25-JUL-1997 ATTORNEY/AGENT INFORMATION: NAME: CALING, ECA'IN P. REGISTRATION NUMBER: 34,090 REFERENCE/POCKET UNBER: DX0758K1 TELECOMMUNICATION: (650)852-9196
 Score 1000; DB 2;
Pred. No. 4.7e-106;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 99.64;
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74.68;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 196 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 74.61
Matches 141; Conservative
Query Match
Best Local Similarity 99.5
Matches 188; Conservative
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                                                                                                                                                                                                                                                                              181 AHGAATLSP 189
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60 GDEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMD-LREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09935366A
Sequence No. RE39015
GENERAL INFORMATION:
APPLICANT: Bazan, J. Fernando
AITLE OF INVENTION: MAWMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Indels
                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 718.5; DB 2;
; Pred. No. 7.3e-74;
14; Mismatches 33;
                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/558,474
FILING DATE: 25-Apr.2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION UNMBER: US 60/053,765
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                              ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (650)852-9196
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                                       CITY: Palo Alto
STATE: California
COUNTRY: USA
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COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 74.6%
Matches 141; Conservative
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US-09-935-366A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 EDEETKONNVPRIQCEDGCDPQGLKDNSQFCLQRIRQGLAFYKHLLDSDIFKGEPALLPDS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 PVAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 PMEQLHTSLLGLSQLLQPEDHPRETQQMPSLSSSQQWQRPLLRSKILRSLQAFLAIAARV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMD-LREE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 196;
                                Sequence 4, Application US/09558087
Patent No. 649567
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09558474
Patent No. 6835825
GENERAL INFORMATION
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
                                                                                                                                                                                                                                                            COUNTY: USA

ZIP: 94304-1104

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/558,087

FILING DATE: 25-Apr-2000

CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .3e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 71.6%; Score 718.5; Best Local Similarity 74.6%; Pred. No. 7.3e Matches 141; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/053,765 FILING DATE: 25-UUL-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ching, Edwin P. REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                         CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 FAHGAATLT 189
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8; Indels

DB 2; Length 102;

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89 CLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSPVAQLHASLLGLSQLLQPEGHHWETQQIP 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09558089
Patent No. 6479634
GENERAL INFORMATION:
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IPM PC compatible

COMPUTER: IPM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOSTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/558,089

FILING DATE: 25-Apr-2000

CLASSIFCATION: cUnknown>

PRIOR APPLICATION DATA:

APPLICATION DATA:

ATTORNEY/AGENT INPORMATION:

NAME: CHING BATE: cunknown>

ATTORNEY/AGENT INPORMATION:

NAME: CHING: Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: 30,090

REFERENCE/DOCKET NUMBER: 30,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 SLSPSOPWORLLLRFKILRSLOAFVAVAARVFAHGAATLS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 46.1%; Score 463; DB 2; Best Local Similarity 90.0%; Pred. No. 4.7e-45; Matches 90; Conservative 2; Mismatches E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
APPLICATION NUMBER: US 60/053,,,,,
FILING DATE: 25-JUL-1997
ATTORNEY, AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE, DOCKET NUMBER: DX0758K1
TELECHONE: (650)852-9196
TELEPAN: (650)852-9196
INFORMATION FOR SEQ 10 NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
LENGTH: amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (650)496-1200 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-558-089-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 PVAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MLDCRAVIMLWLLPWVTQGLAVPRSSSPDWAQCQQLSRNLCMLAWNAHAPAGHMNLLREE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMD-LREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Bazan, J. Fernando
TITLE OF INFORMATION:
MUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alco
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPALIALE
COMPUTER: ISM PC COMPATION SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 196;
                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/935,366A
FILING DATE: 22-Aug-2001
CLASSIFCATION NUMBER: 09/122,443
PRIOR APPLICATION NUMBER: 09/122,443
PRIOR APPLICATION NUMBER: 09/122,443
FILING DATE: cUnknown-
PRIOR APPLICATION NUMBER: 09/122,443
FILING DATE: CUNKNOWN-
NAME: CLING, EGAHIN P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECAMINICATION INVORMATION:
TELECAMINICATION INVORMATION:
TELECAMINICATION SOR SEQ. 10 96
TELEFAX: (650)496-1200
INFORMATION FOR SEQ. 1D NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.6%; Score 718.5; DB 6; Length 74.6%; Pred. No. 7.3e-74; tive 14; Mismatches 33; Indels
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ELLOATION NUMBER: US/09/122,443
FILING DATE: 24-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-935-366A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-09-122-443-5
; Sequence 5, Application US/09122443
; Patent No. 6060284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 196 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 74.6
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 24-JUL-
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 FAHGAATLS 188
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                                                                                                                                                                     2 CLORIHOGLVFYEKLIGSDIFTGEPSLHPDGSVGQLHASLLGLRQLLQPEGHHWETEQTP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CLORIHOGLVFYEKLIGSDIFTGEPSLHPDGSVGOLHASLLGLROLLOPEGHHWETEQTP 61
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                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09558087
Patent No. 6495667
GENERAL INFORMATION
GENERAL INFORMATION: ADMINISTRATED REAGENTS
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                            Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPER PROPRY
(COMPUTER: PORM:
MEDIUM TYPER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/558,087
FILING DATE: 25-Apr-2000
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 102
                                                                                                                             89 CLORIHOGLIFYEKLLGSDIFTGEPSLLPDSPVAQLHASLLGLSQLLQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                     Indels
                                                                                                                                                                                                                                         62 SPSPSQPWQRLLLRLKILRSLQAFVAVAARVFAHGAATLS 101
                                                                                                                                                                                                                149 SLSPSOPWORLLLRFKILRSLOAFVAVAARVFAHGAATLS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 SLSPSQPWQRLLLRFKILRSLQAFVAVAARVFAHGAATLS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 SPSPSQPWQRLLLRRKILRSLQAFVAVAARVFAHGAATLS 101
                                        46.1%; Score 463; DB 2;
ilarity 90.0%; Pred. No. 4.7e-45;
Conservative 2; Mismatches 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
46.1%; Score 463; DB 2;
Best Local Similarity 90.0%; Pred. No. 4.7e-45;
Matches 90; Conservative 2; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/053,765
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
TREFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-558-087-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acids
                                        Query Match
Best Local Similarity
Matches 90; Conserv
                                                                                                                                                                                                                                                                                                                           RESULT 14
US-09-558-087-5
US-09-558-089-5
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89 CLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSPVAQLHASLLGLSQLLQPEGHHWETQQIP 148
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Sequence 5, Application US/09558474

Patent No. 6835825
GENERAL INFORMATION:
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSES: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                 CITY: Palo Alto
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
CONFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
CORPUTER: SYSTEM: PC -DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/558,474
FILING DATE: 25-Apr-2000
CLASSIFICATION NUMBER: US/09/558,474
FILING DATE: 25-Apr-2000
RIOR APPLICATION NUMBER: US/0003,765
FILING DATE: 25-UUL-1997
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 463; DB 2; Length 102;
Pred. No. 4.7e-45;
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REGIGTRATION NUMBER: 34,090
REGIGTRATION NUMBER: DX0758K1
TELECOMMUNICATION INPORMATION:
TELECHONE: (650) 852-9196
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HOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-558-474-5
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Best Local Similarity 90.0%;
Matches 90; Conservative
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181 AHGAATLSP 189
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/EMC_Celerra_SIDS3/prodata/2/pubpaa/US08_PUBCOMB.pep:*
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/EMC_Celerra_SIDS3/prodara/2/pubpaa/US10A_PUBCOMB.pep:*
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1004
1 MLGSRAVMLLLLLPWTAQGR......QAFVAVARVFAHGAATLSP 189
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	
232,	232,	232,	232,	232,	232,	232,	232,	232,	232,	232,	232,	232,	232,	232,	232,	232,	232,	
Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	
US-10-123-236-232	US-10-123-261-232	US-10-140-921-232	US-10-140-928-232	US-10-121-045-232	US-10-123-292-232	US-10-123-903-232	US-10-124-819-232	US-10-124-822-232	US-10-140-925-232	US-10-160-498-232	US-10-124-824-232	US-10-127-825A-232	US-10-127-829A-232	US-10-127-835A-232	US-10-127-839A-232	US-10-127-901A-232	US-10-128-693A-232	
4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	
189	189	189	189	189	189	189	189	189	189	189	189	189	189	189	189	189	189	
9.66	9.66	9.66	9.66	9.66	9.66	9.66	9.66	99.6	9.66	9.66	9.66	9.66	9.66	9.66	9.66	9.66	9.66	
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61 DEETTINDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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                                                                                               GENERAL LINEARANION STATEMENT APPLICANT: De Waal Malefyt, Rene
APPLICANT: Lira, Sergio A.
APPLICANT: Lira, Sergio A.
APPLICANT: Lira, Sergio A.
APPLICANT: Oppmann, Birgit
APPLICANT: Rennick, Donna M.
APPLICANT: Rennick, Donna M.
APPLICANT: Rennick, Donna M.
APPLICANT: Rennick, Donna M.
APPLICANT: Wiekowski, Maria
ITILE OF INVENTION: Mammalian Cytckines; Related Reagents and Methods
FILE REFERENCE: DX01042X US
CURRENT PELLON NUMBER: US/10/375,706
CURRENT FILING DATE: 2000-09-08
FRIOR APPLICATION NUMBER: US/09/658,699
FRIOR APPLICATION NUMBER: 09/393,090
FRIOR PILING DATE: 1999-09-09
FRIOR PILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver: 2.1
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Pred. No. 1.7e-95;
Mismatches 0;
US-10-375-706-2
; Sequence 2, Application US/10375706
; Seulication No. US20030162261A1
; GENERAL INFORMATION:
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ORGANISM: Unknown Organism
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Best Local Similarity 100.
Matches 189; Conservative
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RESULT 5
US-11-006-154-2
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| Publication No. US20040223969A1
| Publication No. US20040223969A1
| GENERAL INPOWARTON:
| APPLICANT: Oft, Martin
| APPLICANT: Oft, Martin
| TITLE OF INVENTION: USES OF IL-23 AGONISTS AND ANTAGONISTS; RELATED REAGENTS
| TITLE REFERENCE: DXG6022US01
| CURRENT APPLICATION NUMBER: US/10/797,157
| CURRENT FILING DATE: 2004-03-09
| PRIOR FILING DATE: 2003-03-10
| NUMBER OF SEQ ID NOS: 11
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 2
| LENGTH: 189
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APPLICANT: Chan, Jason R.
APPLICANT: Chan, Jason R.
APPLICANT: Moore, Kevin
APPLICANT: Nguyen, Nhung
APPLICANT: Churakova, Tatyana
APPLICANT: Chan, Shi-Juan
APPLICANT: Cua, Daniel J.
TITLE OP INVENTION: Uses of mammalian cytokine; related reagents
FILE REFERENCE: DX01578K
CURRENT APPLICATION NUMBER: US/10/742,405
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.2
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Best Local Similarity 100.0%; Pred. No. 1.7e-95;
Matches 189; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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100.0%; Pred. No. 1.7e-95;
tive 0; Mismatches 0;
                                                                                      ; Sequence 4, Application US/10742405; Publication No. US20040213761A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 189; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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APPLICANT: Chirica, Madaline
APPLICANT: Chirica, Madaline
APPLICANT: Parham, Christi L.
APPLICANT: Rastelein, Robert A.
APPLICANT: Restelein, Robert A.
APPLICANT: Mammalian Receptor Proteins; Related Reagents and Methods.
TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
TITLE OF INVENTION: WINBER: US/10/720,026
CURRENT APPLICATION NUMBER: US/10/720,026
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Version 3.2
SEQ ID NO 6
LENGTH: 189
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                                                                                                                                              61 DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLFYEKLLGSDIFTGEPSLLPDSP 120
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                             1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
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; Publication No. US20050158750A1
; GENERAL INFORMATION:
    APPLICANT: Bazan, J. Fernando
    TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; CORRESPONDENCES 16
; CORRESPONDENCE ADDRESS:
; STREET: 901 California Avenue
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100.0%; Pred. No. 1.7e-95;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 189; Conservative
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APPLICANT: Evans, Cheryl
APPLICANT: Morberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Applicant: Applicant: Applicant: Spanding vikki
APPLICANT: Spanding vikki
APPLICANT: Spanding vikki
APPLICANT: Spanding vikki
APPLICANT: Clark, Hilary
APPLICANT: Clark, Hilary
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6075-834
CURRENT PILIOR DATE: 1999-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLGSRAVMLLLLEPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020187523A1 2933038CD1
US-09-965-528-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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Best Local Similarity 99.5%; Pred. No. 4.4e-95;
Matches 188; Conservative 0; Mismatches 1;
                             PRIOR APPLICATION NUMBER: 60/134, 949
PRIOR FILING DATE: 1999-05-19
PRIOR PELING DATE: 1999-07-15
PRIOR PELING DATE: 1999-07-15
PRIOR APPLICATION NUMBER: 60/146, 700
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 138, Application US/09374046A Publication No. US20030096951A1 GENERAL INFORMATION:
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APPLICANT: McCoy, JOHD M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa
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SOFTWARE: PatentIn Ver. 2.0
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US-09-374-046A-138
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ORGANISM: Homo sapiens
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CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-104
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/006,154
FILING DATE: 06-Dec-2004
CLASSIFICATION: AUNKNOWN>
PRIOR APPLICATION: AUNKNOWN>
PRIOR APPLICATION NUMBER: US/09/935,366
FILING DATE: 22-Aug-2001
APPLICATION NUMBER: 09/122,443
FILING DATE: CALURIOWN:
NAME: CALUR BATE: AUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: CALUR BATE: AUNKNOWN>
REFERENCE/DOCKET NUMBER: BX0758K1
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
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| Sequence 14, Application US/09965528
| Publication No. US20020187523A1
| GENERAL INFORMATION |
| APPLICANT: INCYTE GENOMICS, INC. |
| APPLICANT: TANG, Y. Tom |
| APPLICANT: USC, Henry |
| APPLICANT: BURFORD, Neil |
| APPLICANT: BURFORD, Neil |
| APPLICANT: BAUGHN, Mariah R. |
| APPLICANT: BAUGHN, Mariah R. |
| APPLICANT: AZIMZI, Yalah M. |
| APPLICANT: PATTERSON, Chandra |
| APPLICANT: PATTERSON, Chandra |
| APPLICANT: PATTERSON, Chandra |
| APPLICANT: LU, Dyung Aina M. |
| APPLICANT: PATTERSON, CHANDRA |
| APPLICANT: PATTERSON, CHANDRA |
| FILE REFERENCE: PF-0701 USA |
| CURRENT APPLICATION NUMBER: US/09/965,528
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HOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-11-006-154-2
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FITLE OF INVENTION:
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APPLICANT:
APPLICANT:
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                                                                                                                      1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG 60
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APPLICANT: LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
FILE REFERENCE: PF-0701-1 USA
CURRENT APPLICATION NUMBER: US/09/969,984
CURRENT FILING DATE: 2001-10-02
PRIOR PAPLICANTON NUMBER: 60/134,949; 60/144,270; 60/146,700; 60/157,508
PRIOR FILING DATE: 1999-05-19; 1999-07-15; 1999-07-30; 1999-10-04
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PERL PROGram
                                                                             1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
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                              Gaps
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99.6%; Score 1000; DB 3; Length 189;
Best Local Similarity 99.5%; Pred. No. 4.4e-95;
Matches 188; Conservative 0; Mismatches 1; Indels
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; OTHER INFORMATION: Incyte ID No. US20040048244A1 2933038CD1
US-09-969-984-14
                              1; Indels
  99.5%; Pred. No. 4.4e-95; ive 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: TANG, Y. Tom
APPLICANT: YUE, Henry
APPLICANT: LAL, Preet;
APPLICANT: BAURMAN, Olga
APPLICANT: BAURMAN, Olga
APPLICANT: AZIMZAI, Yalda
                              Conservative
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Best Local Similarity
Matches 188; Conserv
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US-09-969-984-14
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LENGTH: 189
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FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
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PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059112
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059189
PRIOR PELING DATE: 1997-09-19
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R APPLICATION NUMBER: 60/062287
R FILING DATE: 1997-10-17
A PPLICATION NUMBER: 60/062814
R FILING DATE: 1997-10-24
R APPLICATION NUMBER: 60/062816
Application US/10028072
5. US20030004311A1
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PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
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FILING DATE: 1997-10-31
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APPLICATION NUMBER: 60/063327
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APPLICATION NUMBER: 60/063329
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APPLICATION WUBER: 60/063561
FILING DATE: 1997-10-28
APPLICATION NUMBER: 60/063704
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Stewart, Timothy A.
Tumas, Daniel
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Wood, William
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Gerritsen, Mary E.
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                                                                                                                              Beresini, Maureen
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Gurney, Austin L.
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Filvaroff, Ellen
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                                                                                            APPLICANT: Baker, Kevin P.
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R FILING DATE: 1997-12-11
R APPLICATION NUMBER: 60/069334
R FILING DATE: 1997-12-11
R APPLICATION NUMBER: 60/069694
R FILING DATE: 1997-12-16
R APPLICATION NUMBER: 60/072320
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R APPLICATION NUMBER: 60/077791
R APPLICATION NUMBER: 60/07791
R APPLICATION NUMBER: 60/079294
R FILING DATE: 1998-03-25
R FILING DATE: 1998-03-25
R FILING DATE: 1998-03-25
R APPLICATION NUMBER: 60/079693
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R APPLICATION NUMBER: 60/081695
R FILING DATE: 1998-04-14
R FILING DATE: 1998-04-14
R FILING DATE: 1998-04-15
R APPLICATION NUMBER: 60/081818
                                                                            FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063738
FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063755
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APPLICATION NUMBER: 60/664809
FILING DATE: 1997-11-07
APPLICATION NUMBER: 60/065186
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FILING DATE: 1997-11.24
APPLICATION NUMBER: 60/066511
FILING DATE: 1997-11.24
APPLICATION NUMBER: 60/066770
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FILING DATE: 1998-02-04
APPLICATION NUMBER: 60/074086
FILING DATE: 1998-02-09
APPLICATION NUMBER: 60/074092
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APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/080165
FILING DATE: 1998-03-31
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APPLICATION NUMBER: 60/064248
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APPLICATION NUMBER: 60/082999
FILING DATE: 1998-04-24
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FILING DATE: 1997-11-17
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FILING DATE: 1997-11-21
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APPLICATION NUMBER: 60/069212
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APPLICATION NUMBER: 60/069278
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FILING DATE: 1998-04-09
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FILING DATE: 1998-04-28
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DEETTNDVPHIOCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120 1 MLGSRAVMILLILPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG 1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG ö Length 189 Indels Score 1000; DB 4; Pred. No. 4.4e-95;); Mismatches 1; PRIOR APPLICATION NUMBER: 60/08549
PRIOR FILING DATE: 1998-05-07
PRIOR PELLING DATE: 1998-05-12
PRIOR PELLING DATE: 1998-05-13
PRIOR PELLING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-13
PRIOR PELLING DATE: 1998-05-13
PRIOR PELLOR NUMBER: 60/08559
PRIOR PELLING DATE: 1998-05-15
PRIOR PELLING DATE: 1998-06-10
PRIOR PELLING DATE: 1998-06-24
PRIOR PELLING DATE: 1998-06-24
PRIOR PELLING DATE: 1998-06-24
PRIOR PELLING DATE: 1998-06-24
PRIOR PELLING DATE: 1998-06-26
PRIOR PELLING DATE: 1998-06-20
.. Query Match
Best Local Similarity 99.5%;
Matches 188; Conservative 61 61 ઠે පු 셤 ઠ

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                                                                                             APPLICANT: Stewart, Timochy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENOUGH THE SAME
TITLE OF INVENTION: UNMERR: US/10/121,049
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US/10/121,049
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SCRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACCIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 232, Application US/10123904
Publication No. US20030022328A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
                                                         Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
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Watanabe, Colin K
Wood, William
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Goddard, Audrey
                     Godowski, Paul J.
Gurney, Austin L.
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Sherwood, Steven
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Filvaroff, Ellen
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US-10-121-049-232
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LENGTH: 189
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APPLICANT:
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99.6%; Score 1000; DB 4; Length 189;
Best Local Similarity 99.5%; Pred. No. 4.4e-95;
Matches 188; Conservative 0; Mismatches 1; Indels
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Sequence 213, Application US/10121049

Sequence 213, Application US/10121049

Publication No. US2003002223941

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeBroyers, Luc

APPLICANT: Trivaroff, Rilen

APPLICANT: Gao, Wei-Oiang

APPLICANT: Gao, Wei-Oiang

APPLICANT: Gao, Wei-Oiang
                                                                                                                                          ; Sequence 232, Application US/10140808; Publication No. US20030017563A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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Pilvacef, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Peul J.
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181 AHGAATLSP 189
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181 AHGAATLSP 189
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ORGANISM: Homo Sapien
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121 VAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVF 180
                                                         DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RLG353
CURRENT APPLICATION NUMBER: US/10/175,746
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Watanabe, Colin K
Wood, William
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Filvaroff, Ellen
Gao, Wei-Qiang
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US-10-175-746-232
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US-10-175-746-232
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330ACLG:
CURRENT APPLICATION NUMBER: 10/10/140,470
CURRENT FILING DATE: 2002-05-06
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99.6%; Score 1000; DB 4; Length 189;
Best Local Similarity 99.5%; Pred. No. 4.4e-95;
Matches 188; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                         Query Match

99.6%; Score 1000; DB 4; Length 189;
Best Local Similarity 99.5%; Pred. No. 4.4e-95;
Matches 188; Conservative 0; Mismatches 1; Indels
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EQ ID NO 232
LENGTH: 189
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Tumas, Daniel
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Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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Filvaroff, Ellen
Gao, Wei-Qiang
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Smith, Victoria
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                                                         ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-232
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ORGANISM: Homo Sapien
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APPLICANT: DeForge, Laura
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Oiang
APPLICANT: Gao, Wei-Oiang
APPLICANT: Gao, Wei-Oiang
APPLICANT: Gao, Wei-Oiang
APPLICANT: Gadowski, Paul J.
APPLICANT: Garwod, Steven
APPLICANT: Shewood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Watenabe, Colin K.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLGSRAVMLLLLEPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHWDLREEG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQXLCTLAWSAHPLVGHMDLREEG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

99.6%; Score 1000; DB 4; Length 189;
Best Local Similarity 99.5%; Pred. No. 4.4e-95;
Matches 188; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: June 20, 2006, 04:46:39
Job time : 139.436 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Homo Sapien
US-10-176-918-232
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June 20, 2006, 04:42:09; Search time 12.7636 Seconds (without alignments) 334.012 Million cell updates/sec
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| EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*
| FMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*
| FMC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:*
| FMC Celerra SIDS3/ptodata/2/pubpaa/US08 NEW PUB.pep:*
| FMC Celerra SIDS3/ptodata/2/pubpaa/US08 NEW PUB.pep:*
| FMC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*
| FMC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*
| FMC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*
| FMC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*
                                                                                                                                                                                                                                                             US-10-797-157-2
1004
1 MLGSRAVWLLLLLPWTAQGR......QAFVAVARVFAHGAATLSP 189
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   96747 segs, 22556637 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                                                                                                          protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                Title:
Perfect score:
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Maximum DB
                                                                                                          OM protein
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                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 22338, A Sequence 36507, A Sequence 11452, A Sequence 11452, A Sequence 50055, A Sequence 50055, A Sequence 1507, A A Sequence 1406, A B Sequence 1406, A B Sequence 1406, A B Sequence 55377, A Sequence 3667, A B S	
US-10-953-349-22338 US-10-449-902-50312 US-10-953-349-11454 US-10-953-349-11454 US-10-953-349-11455 US-10-49-902-50055 US-10-49-902-50055 US-10-449-902-5005 US-10-49-902-56207 US-10-953-349-1407 US-10-953-349-1405 US-10-953-349-1405 US-10-953-349-1405 US-10-953-349-1405 US-10-953-349-1405 US-10-953-349-1405 US-10-953-349-1405 US-10-953-349-1405 US-11-293-697-567 US-11-293-697-67	US-10-505-928-453 US-10-511-937-2489 US-10-933-854-11
34622 35746 35746 35746 35746 3738 3738 3677 3677 3677 3677 3677 367	212 6 212 6 212 6 212 6
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69 69 67 67 67 67 67 67 67 67 67 67 67 67 67	999
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	1 4 4 4 1 W 4 R

ALIGNMENTS

RESULT 1

OUS-10 SEQUENCE OF THE PROPERTY OF THE PROPER	US-10-511-937-2461 US-210-511-937-2461 Sequence 2461, Application US/10511937 Sequence 2461, Application US/10511937 Sequence 2461, Application NO. US200608836A1 APPLICANT: ENCRWAITION: APPLICANT: Mocdward, Nobert APPLICANT: Mocdward, Robert APPLICANT: Mocdward, Robert APPLICANT: Mocdward, Robert APPLICANT: No Secuence 25 Steven APPLICANT: Mocdward, Nobert APPLICANT: No NOBER: US/10/511,937 CURRENT APPLICATION NUMBER: US/10/511,937 CURRENT APPLICATION NUMBER: US/10/511,937 CURRENT APPLICATION NUMBER: US/10/311,831 PRIOR PILING DATE: 2003-04-24 PRIOR PILING DATE: 2003-04-24 PRIOR PILING DATE: 2003-04-24 PRIOR FILING DAT
g	83SLGIPWAPL-SSCPSQALQLAGCLSQL#SGL#LYQSLLQALEGISF
& g	114 SLLPDSPVAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKI

11;

113 127 165 183

82

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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: EXTYNEOPOLETIN: REMODELING AND
TITLE OF INVENTION: GLYCOCONUGATION OF ERYTHROPOLETIN
TITLE OF INVENTION: GLYCOCONUGATION OF ERYTHROPOLETIN
FILE REFERENCE: 040833-01-5083-012
CURRENT APPLICATION NUMBER: US 10/410,945
PRIOR PILING DATE: 2005-07-15
PRIOR PELICATION NUMBER: US 10/410,945
PRIOR FILING DATE: 2002-09-28
PRIOR FILING DATE: 2002-09-28
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-17
PRIOR FILING DATE: 2002-09-17
PRIOR PELING DATE: 2002-06-17
PRIOR FILING DATE: 2002-06-17
PRIOR FILING DATE: 2002-06-17
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                     APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryne
                                                                                                                                                                                                   Sequence 2, Application US/11183218
Publication No. US20060088906A1
GENERAL INFORMATION:
                                 ||:|: |: || |
184 ASHLQSFLEVSYRVLRH 200
166 LRSLOAFVAVAARVFAH 182
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US-11-183-218-2
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ORGANISM:
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RESULT 3

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Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 VPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTG-EPSLLPDSPVAQLHA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

FILING DATE: 10-Sep-2002

APPLICATION NUMBER: US/08/797,689

FILING DATE: 31-JAN-1997

APPLICATION NUMBER: US 08/256,927

FILING DATE: 28-JUL-1994

APPLICATION NUMBER: R 92/01064

FILING DATE: 31-JAN-1992

APPLICATION NUMBER: PC 7/PR93/00085

FILING DATE: 31-JAN-1993

APPLICATION NUMBER: PCT/FR93/00085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/330,353
FILING DATE: 12-Jan-2006
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Sequence 14, Application US/11330353; Publication No. US20060105429A1; GENERAL INFORMATION: APPLICANT: Fleer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION TELEPHONE: (610) 454-383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 VFAH 182
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429 RVRELAQAAGFAPQTGARPSETFARPCKSQ-----ESALGNIVPAVEPGTPPLDILA 480
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127 SLLGLSQLLQPEGHHWETQQIPSLSPSQ-----PWQRLLLRFKILRSLQAFVAVAAR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 MLLLLLPWTAQGRAV-PGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEGDEETTN
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fry, Kirk, Cay
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Drentice, James
APPLICANT: Prentice, James
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: MAD MONITORING TRANSPLANT REJECTION
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR PILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 7.8%; Score 78.5; DB 6; Best Local Similarity 29.9%; Pred. No. 2.5; Matches 46; Conservative 20; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 Q-LHAS---LLGLSQLLQPEGHHWETQQIPSLSP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPLEASNPALEGLTOPLOGGTPHCEPCOLPSESP 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 4308, Application US/11293697; Publication No. US20060105376A1; Publication No. US20060105376A1; GENERAL INFORMATION:
; ATTLE ATTLE OF INVENTION: Novel full length cDNA; FILE REFERENCE: H1-A0106; CURRENT APPLICATION UNMBER: US/11/293,697; CURRENT FILING DATE: 2002-12-05; PRIOR PELING DATE: 2002-03-28; NUMBER OF SEQ ID NOS: 5458; SEQ ID NO 4308
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
                                                                                                                                                                                                                                                                                   Sequence 2514, Application US/10511937
Publication No. US20060088836A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 3117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-511-937-2514
                                                                                                      179 VFAH 182
                                                                                                                                                       191 VLRH 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-293-697-4308
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                                                                                                                                               Sequence 16, Application US/11330353
Publication No. US20060105429A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
CONTAINING SAID POLYPEPTIDES
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٠<u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 IPWAPL-SSCPSQALQ--LAGCLSQLHSGFFLYQGLL--QALEGISPELGFTLDTLQLDV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 LIKCLEQVRKIQGDGA-----SLQEKLCATYKLCHPEELVLLGH-----SLG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 LLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHP----LVGHMDLREEGDEETTND 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40; Gaps
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9.6%; Score 96; DB 7; Length 787;
Best Local Similarity 26.1%; Pred. No. 0.067;
Matches 48; Conservative 19; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 [Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/330,353
FLING DATE: 12-Jan-2006
CLASSIFICATION ATA:
APPLICATION NUMBER: US/10/237,624
FLING DATE: 10-Sep-2002
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 31-JAN-1997
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1993
ATTORNEY/ARE: 31-JAN-1993
ATTORNEY/ARE: 28-JAN-1993
ATTORNEY/ARE: 28-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Rhone-Poulenc Rorer Inc. STREET: 500 Arcola Road, 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 787 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Collegeville
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                        170 VLRH 173
                                                                                                                               US-11-330-353-16
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APPLICANT: National Institute of Agrobiological Sciences.
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                                                                                                                                                                                                                                                                                                                                   429 RVRELAQAAĞFAPQTGARPSETFARFCKSQ------BSALGNTVPAVEPGTPPLDILA 480
                                                                                                                                                                                                                                                        389 MVHLLIP--ELGACVAPGGN----LIVELARYL------VDVRQEQLQGFNT 428
                                                                                                                                                                                                                                                                                                      67 DVPHIQCGDGCDPQ-GLRDN---SQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSPVA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 AQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVFA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMLG----GIEEMIRSEGIRWVIADV----SMAW-----VTELAATVGVHVALFS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 PHIQCG-----DGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSPV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 VMVLPFPAQGHVMP-----LMELSHRLVGLGFEVEFV--HTDFNRDRVINAMANET 61
                                                                                                                                                                                                             8 MLLLLLPWTAQGRAV-PGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEGDEETTN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 LLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDL-REEGDEETTNDV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 47066, Application US/10449902

Sequence 47066, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement Institution.

APPLICANT: Foundation for Advancement of International Science.

ITILE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

FRIOR FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: UP 2002-203269

PRIOR PRILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-11

NUMBER OF SEQ ID NOS: 56791

SEQ ID NO 47066

LENGTH: 457
                                                                                                                                                               37;
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                                                                                                                   DB 7; Length 541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.8%; Score 78; DB 6; Length 457; Best Local Similarity 21.8%; Pred. No. 2.3; Matches 41; Conservative 26; Mismatches 57; Indels
                                                                                                                                                               51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          481 QPLEASNPALEGLTQPLQGGTPHCEPCQLPSESP 514
                                                                                                                                                                                                                                                                                                                                                                                                 Q-LHAS---LLGLSQLLQPEGHHWETQQIPSLSP 152
                                                                                                              7:8%; Score 78.5; DB 29.9%; Pred. No. 2.5; tive 20; Mismatches
                                                                                                                                                               46; Conservative
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-47066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 -HGAATLS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 TYSAAVVA 145
                                                                                                            Query Match
Best Local Similarity
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Sequence 42967, Application US/10449902 Publication No. US20060123505A1 GENERAL INFORMATION:

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Sequence 14, Application US/11254252

Sequence 14, Application US/11254252

Publication No. US20060110755A1

GENERAL INFORMATION:

APPLICANT: Branzusoff, Alex

APPLICANT: Franzusoff, Alex

APPLICANT: King, Thomas H.

TITLE OF INVENTION: YEAST-BASED THERAPEUTIC FOR CHRONIC HEPATITIS C INFECTION
FILE REFERENCE: 3923-12

CURRENT APPLICATION NUMBER: US/11/254,252

CURRENT PILING DATE: 2005-10-18

PRIOR APPLICATION NUMBER: US 60/620,158

PRIOR APPLICATION NUMBER: US 60/620,158

PRIOR APPLICATION NUMBER: US 60/434,163

PRIOR APPLICATION NUMBER: US 60/434,163

PRIOR APPLICATION NUMBER: US 60/434,163

PRIOR PILING DATE: 2002-12-16

NUMBER OF SEQ ID NOS: 21

SEQ ID NO 14

LENGTH: 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 IVVVDHELPNQGSQQRRIVSFVGGLDLCDGRYDTQYHSLFRTLDSTHHDDFHQPNFATAS 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 ŚNAQHLIYITGWSVYTEITLVRDSNRPKPGGDV---TLGELLKKKACEGVRVLMLVWDDR 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 TSVGL--LKRDGLMATHDEETENYFHGSDVNCVLCPRNPDDSGSIVQDLSISTMFTHHQK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 SRAVMLLLLLPWTA------QGRAVPGGSSPAWTQCQQLSQKLC-----TLAWSAH 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 PLVGHMDLREEG----DEETIN----DVPHIQCGDGCDPQG--LRDNSQFCLQRIHQG 96
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTYON: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT PELING DATE: 2003-629
PRIOR PAPLICATION NUMBER: UP 2002-203269
PRIOR APPLICATION NUMBER: UP 2002-383870
PRIOR PLING DATE: 2002-05-30
PRIOR PLING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SEQ ID NO 42967
LENGTH: 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.8%; Score 78; DB 6; Best Local Similarity 24.2%; Pred. No. 4.7; Matches 48; Conservative 21; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: recombinant fusion protein US-11-254-252-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 IPSLSPSOPWORLLLRFK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                398 İKKGGPREPWHDIHSRLE 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Oryza sativa
US-10-449-902-42967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-11-254-252-14
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                                                                                                                                                                                                                          87 PWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKVIDTLTCGFADLMGYIPLVY 146
                                                                                               ---REEGDEETTNDVPH----IQCGD-----GCDPQGLRDNSQFCLQRIHQGLIFYEKL 103
                                                                                                                                          147 QVRNSSGLYHVTNDCPNSSIVYEAADAILHTPGCVPCVREGNASRCWVAVTPTVATRDGK 206
                                                                                                                                                                                       104 LGS-----DIFTGEPSLLPDSPVAQLHASLLGLSQL--LQPEGHHWETQQIP-SLSPS 153
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Publication No. US20060123505A1

GENERAL InfoRMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: National Institute of Physical and Chemical Research.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Poundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT FILING DATE: 2003-05-29

PRIOR PLILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: UP 2002-203269

PRIOR APPLICATION NUMBER: UP 2002-383870

PRIOR PELING DATE: 2002-12-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 50549, Application US/10449902
Bublication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: National Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
IITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 YEKLLGSDIFTGEPSLLPDSPVAQLHASLLGLSQLLQPEGHHW 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----CRSDEPLALLHGDLCGPITPATPSGNRY 230
                                                                                                                                                                                                                                                                                      154 -----QPWQRL-----LLRFKILRSLQAFVAVAARV 179
                                                                                                                                                                                                                                                                                                                       266 HITGHRMAWDMMMWSPTAALVVAQLLRIPQAIMDMETHV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILLING DATE: 2003-05-29
PRIOR PILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR PLING DATE: 2002-05-30
PRIOR PLING DATE: 2002-12-11
NUMBER OF SEG ID NOS: 56791
SEQ ID NO 50549
14 PWTAQGR-----AVPGGSSPAW-
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US-10-449-902-50549
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ORGANISM:
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Sequence 21468, Application US/10953349
; Publication No. US20060107345A1
; Publication No. US20060107345A1
; APPLICANT: ALEXANDROW, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REPERENCE: 2750-15799US2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
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; Publication No. US20060107345A1
; GENERAL INFORMATION:
; TILLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TILLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                                                                                         60 RVYLBILTIPLFLIGYVIPQGSLVYWTINGLITVAQQLSLKNDAVKKVLGLPDTRAHQKF 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 LEDGTKIAVKRMEHGVISSKAL---EEFQAEIAVL--SKVRHRHLVSLLGYSIDGNERLL 139
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                                                                                                                                                                                                                                                                                                                               5 RAVMLLLLLPWTAQGRAVPGGSSPAWTO-----CQQLSQK------LCTLAWSAH
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                                                                                                                                                                                                                     Length 330;
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                                                                                                                                                                                                                                                                             68; Indels
                                                                                                                                                                                                                        DB 6;
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                                                                                                                                                                                                                     7.6%; Score 76; DB 6
21.8%; Pred. No. 2.5;
tive 21; Mismatches
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SOFTWARE: PatentIn version 3.3
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                                                                                                                                                                                                                                                                             42; Conservative
                                                                                                                ; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-36639
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Best Local Similarity
NUMBER OF SEQ ID NOS SOFTWARE: Patentin V SEQ ID NO 36639
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98 LISWSQGGNEVFVEGSWDNWT----SRRVLEKSGKDHTILLVLPSGVYHYRIIVDGEPK 152
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FILE OF INVENTION: PULL-LENGTH PLANT CDNA AND USES THEREOF FLLE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: UP 2002-203269
; PRIOR APPLICATION NUMBER: UP 2002-303870
; PRIOR APPLICATION NUMBER: UP 2002-303870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 49311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.5%; Score 75; DB (Best Local Similarity 22.9%; Pred. No. 2.7; Matches 44; Conservative 35; Mismatches
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US-10-449-902-49311
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROW, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERNINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15799BUS2
CURRENT FILING DAIE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PARENTIN version 3.3
SEQ ID NO 21466
LENGTH: 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130
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Publication Wo. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: From Company of Physical Agrancement Foundation for Advancement of International Science.
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26.2%; Pred. No. 4.2;
tive 21; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   7.6%; Score 76; DB 6; Length 470;
26.2%; Pred. No. 3.8;
tive 21; Mismatches 35; Indels
           FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTHARE: PatentIn version 3.3
SEQ ID NO 21467
LENGTH: 470
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Matches 32, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32; Conservative
                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-21467
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ORGANISM: Glycine max
US-10-953-349-21466
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Best Local Similarity
Matches 32; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AH 182
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US-10-953-349-21466
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein June 20, 2006, 04:47:05; Search time 143.345 Seconds (without alignments) 602.837 Million cell updates/sec Run on:

189 1 MLGSRAVMLLLLLPWTAQGR.....QAFVAVAARVFAHGAATLSP 189 Perfect score: Sequence:

US-10-797-157-2

Title:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

2589679 seqs, 457216429 residues Searched:

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Word size :

2589342 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post'-processing: Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp1980s:* Geneseq 8:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:*

SUMMARIES

		int	int	int	II.	int	int	int	int	11.	hum	p19	int	hyp	II.	sec	orot	PRO	ext	hum	PRO	PRO	вес	sec
	uo	Human	Human	Human	Human	Human	Human	Human	Human	Human	Novel	Human	Human	Human	Human	Human	SGRF prot	Human	Human	Novel	Human	Human	Novel	Human
	Description	Aaw95002	Aay29783	Aab01981	Aab47120	Abu08268	bg75811	Adf70612	Adq14469	Ads73601	Adv98151	Aea51094	Aeb47331	Adq14473	Ads73607	Aay94966	Aay54606	Aau12287	Aab48070	Abo17731	Abu80985	Abu66685	Abu59766	Abo24956
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de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	6.68	89.9	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0
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ALIGNMENTS

RESULT 1

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Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation; inflammatory condition; drug screening; human.
                                        Human interleukin-B30 (IL-B30) polypeptide.
                                                                                       1. .21
/note= "signal peptide"
                                                                                                         /note= "mature protein"
                                                                                 Location/Qualifiers
   AAW95002 standard; protein; 189 AA.
                            (first entry)
                                                                                                  22. .189
                            21-MAY-1999
                                                                      Homo sapiens
                AAW95002;
                                                                                  Key
Peptide
                                                                                                   Protein
AAW95002
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WO9905280-A1

98WO-US015423. 24-JUL-1998; 04-FEB-1999

97US-00900905. (SCHE) SCHERING CORP. 25-JUL-1997; Bazan JF;

WPI; 1999-142935/12. N-PSDB; AAX17786.

Newly isolated or recombinant polynucleotide encoding mammalian cytokine interleukin-B30 (IL-B30), including fragments - useful for regulating activation, development, differentiation and function of various cell types, and for diagnosing and treating conditions associated with IL-B30.

Claim 2; Page 8-9; 83pp; English.

This represents a human cytokine interleukin-B30 (IL-B30) polypeptide. Host cells containing a vector comprising the IL-B30 nucleic acid are used for the recombinant production of the protein. The polynucleotides

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are useful for diagnosis of IL-B30 mediated conditions, and forensic science (e.g. to distinguish rodent from human, or as a marker to distinguish between different cells exhibiting differential expression or modification patterns). The IL-B30 (including fragments), together with antibodies that bind to IL-B30 are useful for teaching purposes. They are also used for treating conditions associated with abnormal physiology or development, including inflammatory conditions. The polypeptide cytokine should mediate cytokine synthesis and proliferation in cells. IL-B30 is useful for drug screening to identify compounds having binding affinity
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                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 189; DB 2; L 100.0%; Pred. No. 1.4e-172;
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/label= signal
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/label= IL-B30
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N-PSDB; AAZ08865.
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Best Local Similarity
Matches 189; Conserv
                                                                                                                                                                                                                                                                                                                           Sequence 189 AA;
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The present invention describes a composition (I) comprising DNAX

Cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor

subunit I (BSRS1) protein, which together encode a new mammalian cytokine

related receptor (R), or DCRS1 and interleukin B30 (IL-B30) proteins, or

Creaning for ligands (i.e. agonists/antagonists) from a library of

compounds, which are useful for modulating the physiology or development

Compounds, which are useful for modulating the physiology or development

compounds, which evelopment. (R), annibodies and ligands are useful

for treatment of conditions, especially immunological disorders,

associated with conditions exhibiting abnormal expression of (R). (R) is

useful as a phosphate labeling enzyme to label substrates, and the

subunite BSRS1 and DCRS1 are useful as immunogens for generating

antibodies, or as antigens for binding antibodies. Nucleic acids encoding

CR) are useful for identifying related DNAs and mRNAs, and variants from

other individuals or species. The present sequence represents the

specifically claimed human IL-B30, for use in the composition of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
receptor subunits useful in the treatment inflammatory disorders.
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                                    Claim 2; Page 26-27; 133pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AHGAATLSP 189
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                                                                                                                                                                                                                                                                                                                                                                                                              present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 189 AA;
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(SCHE ) SCHERING CORP.
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N-PSDB; AAC85540.
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                                                                                                                                                                                        WO200118051-A2
                                                                                                                                                                                                                                                                                                                                           Oppmann B, De
Wiekowski MT,
                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                       09-SEP-1999;
10-NOV-1999;
                                                    Castleman's
                                                                                                                                                                                                                   15-MAR-2001
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                                                                                                                       Peptide
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                                                                                                                                                                                                                         This sequence represents human interleukin-B30 (IL-B30). IL-B30 is a novel cytokine, exhibiting significant homology to IL-6 and GCSF (granulocyte collony stimulating factor). Cytokines play a critical role in signalling between immune or other cells during an immune response. The precise role if IL-B30 is not yet known - it is likely to have either a stimulatory or an inhibitory effect on haematopoietic cells such as T-cells, B-cells, natural killer (NK) cells and macrophages. Alternatively, it may affect vascular physiology or development, or have neuronal effects. IL-B30, its fragments IL-B30 nucleotides, agonists and canagonists are useful in the diagnosis and treatment of disorders associated with abnormal expression or activity of IL-B30 e.g., inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are useful for recombinant expression of IL-B30 in a host cell, and as a customer of probes and primers. The IL-B30 in a host cell, and as a cource of probes and primers. The IL-B30 suches con be used to detect levels of IL-B30 expression in samples from patients suspected of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may also be used to identify homologous genes in other species. IL-B30 corrected or protein or its fragments are useful as antigens for raising antibodies to various linear and conformational epitopes. Such antibodies may be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DEETTNDVPHIQCGDGCDPQGLRDNSQPCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP
                                                                                                                                              Novel recombinant DNA encoding cytokines especially interleukin-B30 useful as probes or primers for diagnosing immune disorders including autoimmune or chronic inflammatory conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 189; DB 3; Length 189; Pred. No. 1.4e-172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               various linear and conformational epitopes. Su
to detect levels of IL-B30 protein in a sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Scor.
100.0%; Pred. No. ..
0; Mismatches
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                                                                                                                                                                                                     Claim 1; Col 5-8; 32pp; English
98US-00122443
                         97US-0053765P
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Best Local Similarity 100.
Matches 189; Conservative
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                                                    (SCHE ) SCHERING CORP
                                                                                                         WPI; 2000-364420/31.
                                                                                                                       N-PSDB; AAA52577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 189 AA;
24-JUL-1998;
                        25-JUL-1997;
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                                                                               Bazan JF;
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the substantially pure polypeptide comprising a number of distinct segments of a ubstantially pure polypeptide comprising a number of distinct segments of a tleast 7 contiguous amino acids from IL-12 p40 and/or IL-830, and a substantially pure polypeptide comprising a segment of at least 1.

Configuous amino acids from IL-12 p40 and/or IL-830, and a configuous amino acids from IL-12 p40 and/or IL-830. The composition is configuous amino acids from IL-12 p40 and/or IL-830. The composition is useful for modulating physiology or development of a cell or tissue in a configuous amino acids from IL-12 p40 and/or IL-830. The composition of Interferon-gamma (FRNgamma), an enhanced Th1 response such as anti-tumour effect, adjuvant effect, anti-viral effect or antagonized allergic configuration of memory T-cells. An agonist is useful inducing the protein is useful for modulating the trafficking or activation of an inflammatory condition, tissue specific autoimmunity, degenerative cutoimmunity, rheumatory condition, tissue specific autoimmunity, degenerative cutoimmunity, rheumatory condition, tissue specific autoimmunity, degeneration an inflammatory condition, tissue specific autoimmunity, and transplant, spinal injury, stroke, neurodegeneration, an cutoimmunity, rheumatory condition, and inflammatory condition, and inflammatory condition, and condition, and configuration of a transplant, spinal injury, stroke, neurodegeneration, an inflammatory condition is useful as an immunogen for the production a disease, is infections disease, postmenopausal osteoporosis or IL-6 associated antisera or antibodies specific for binding immunogen for the production a antisera or antibodies specific for binding
memory T-cell; leukocyte; rheumatoid arthritis; osteoarthritis; atherosclerosis; multiple sclerosis; vasculitis; spinal injury; delayed hypersensitivity; skin graft; transplant; cancer; tumour; stroke; neurodegeneration; ischaemia; postmenopausal osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DESTINDVPHIQCGDGCCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition comprising interleukin-12 p40 and IL-B30 polypeptide or its segment, useful for ameliorating rheumatoid arthritis, osteoarthritis, atherosclerosis, multiple sclerosis, vasculitis and tumor.
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100.0%; Pred. No. 1.4e-172;
ive 0; Mismatches 0;
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I, Lira SA, Narula SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Matches 189; Conservative
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Length 189 Indels

100.0%; Score 189; DB 6; L 100.0%; Pred. No. 1.4e-172; ive 0; Mismatches 0;

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DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSF 120
                                                                                       1 MLGSRAVMILLILPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
                                                                      1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
                                                                                                                                                  61 DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQCLIFYEKLLGSDIFTGEPSLLPDSP
                                           Matches 189; Conservative
            Query Match
Best Local Similarity
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                                              Binding compounds comprising antibodies which bind to Interleukin B30, useful for treating disorders associated with hematopoietic cells, e.g. inflammation and autoimmune diseases and development disorders.
DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP
                             VAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVF
                                                                                                                                                                                                                                                                                                          Human; interleukin-B30; IL-B30; inflammation; lymphoid cell; immunosuppressive; autoimmune disorder; immunomodulatory; autoimmune disorder; immunomodulatory; anti-inflammatory; vascular, neuroprotective; immunological response; hacematopoietic cell disorder; vascular physiology; development.
                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .21
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                          ABU08268 standard; protein; 189 AA.
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                                                                                                                                                                                                                                                                                Human interleukin-B30, IL-B30.
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98US-00122443.
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                                                                                    AHGAATLSP 189
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AHGAATLSP 189
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N-PSDB; ABX13358.
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24-JUL-1998;
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                                                                                                                                                                                                                       ABU08268;
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VAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVF 180
              Human, antigenic, cytokine, interleukin-B30; IL-B30; protein therapy;
inflammatory condition, autoimmune disorder; activation, development;
differentiation, function; haematopoietic cell; lymphoid cell; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention discloses an isolated antigenic mature polypeptide that is a mammalian cytokine designated interleukin-B30 (IL-B30). The IL-B30 polypeptide is useful for diagnosing or treating (e.g. protein therapy) conditions associated with abnormal physiology or development (e.g. inflammatory conditions or autoimmune disorders), or in regulating the activation, development, differentiation and function of haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New interleukin-B30 (IL-B30) polypeptide, useful for diagnosing or treating e.g. inflammatory conditions or autoimmune disorders, or in regulating the development of hematopoietic cells or lymphoid cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                           22. 189
/label= Mature_IL-B30_protein
                                                                                                                                                                                                                                                                                                                                                                                                                 1. .21
/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                        antiinflammatory; immunosuppressive
                                                                                                                                                                    ABG75811 standard; protein; 189 AA.
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                                                                                                                                                                                                                                                           Human interleukin-B30 (IL-B30).
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98US-00122443.
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                                                           189
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N-PSDB; ABX11988.
                                                           AHGAATLSP
                                                                                       AHGAATLSP
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Sequence 189 AA;

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Seguence 189 AA;
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                                                                                                                                                       61 DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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cells or lymphoid cells. The IL-B30 polypeptide is also useful as an immunogen for producing antisera or antibodies specific for binding. The sequence presented is the human IL-B30 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition comprising fragments from interleukin (IL)-12 p40 and IL-B30 polypeptides is useful to enhance anti-viral, anti-tumor and vaccine effects and to antagonize allergic responses.
                                                                                                                                                                                                                                                                                                                                                                                     interleukin B30; IL-B30; IL-12 p40; tumour necrosis factor alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a composition comprising polypeptide fragments from interleukin (II)-12 p40 and IL-B30 is new. The fragments comprise or 11 contiguous amino acids. Also included are an isolated or recombinant nucleic acid (NI) encoding the polypeptides of the novel
                                                                                                     1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
                                                                                                                  1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                              IFN-alpha; interferon alpha; chronic inflammatory condition; memory T-cell; tumour; anti-viral; vaccine; allergic responses; autoimmune disease; multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease; psoriasis.
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                                                            Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kastelein RA;
                                                            Score 189; DB 6; Length 1; Pred. No. 1.4e-172; 0; Mismatches 0; Indels
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I, Lira SA, Narula SK;
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                                                                                                                                                                                                                                                                                                    ADF70612 standard; protein; 189
                                                           Query Match
Best Local Similarity 100.0%;
Matches 189; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-SEP-1999; 99US-0153281P.
10-NOV-1999; 99US-0164616P.
08-SEP-2000; 2000US-00658699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-FEB-2003; 2003US-00375706.
                                                                                                                                                                                                                                                                                                                                                                 Human interleukin B30.
                                                                                                                                                                                                                               AHGAATLSP 189
                                                                                                                                                                                                                                                 181 AHGAATLSP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SCHE ) SCHERING CORP.
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                                          Sequence 189 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oppmann B, De
Wiekowski MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                             12-FEB-2004
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composition, a cell comprising recombinant N1, a nucleic acid which hybridises the natural coding portion of primate IL-12 p40 and primate IC-30, an antagonist of IL-12 p40/IL-B30 (combined with a tumour necrosis factor (TNF) alpha antagonist, an IL-12 antagonist, IL-10 or steroids), a binding compound comprising an antigen binding site from an antibody which specifically binds to the novel composition, producing of acell or tissue (comprising contacting the cell with the claimed composition to increase production of IFN-alpha, modulating physiology or development of a cell in a host organism (comprising administering the novel composition which results in an anti-tumour, adjuvant, anti-viral or antagonised allergic effect), administering the IL-12 p40/IL-B30 antagonist resulting condition, increasing secretion of a primate IL-B30 (comprising expressing IL-12 p40 with IL-B30, secretion of IL-12 p40 comprising expressing IL-12 p40 with IL-B30, secretion of IL-12 p40 comprising expressing IL-B30 with IL-B30, secretion of IL-12 p40 administering IL-B30 or its agonist. The invention is useful in an animal and inducing the proliferation of memory T-cells by comprising the comprising conditions as associated with abnormal physiology including inflammatory conditions associated with abnormal physiology including inflammatory conditions as associated with abnormal physiology including inflammatory conditions or sociated responses and teaching IL-B30 including inflammatory anti-viral and vaccine responses and teaching IL-B30 including inflammatory conditions or susful to treat autoimmune diseases such as multiple sclerosis or psoriasis or chronic inflammatory souditions such as rheumatoid arthritis proper and pagentic associated sequence represents human IL-
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100.0%; Pred. No. 1.4e-172;
ive 0; Mismatches 0;
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/note= "Signal peptide"
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"Signal peptide"

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Peptide
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                                                                                                                                                                                                                    The invention relates to a novel method for treating or improving wound healing. The method comprises administering to a subject an agonist or antagonist of interlewin (IL)-23. The invention further comprises: an agonist of IL-23 derived from the binding site of an antibody that specifically binds to an IL-23 receptor; and a kit comprising the agonist and a compartment or instructions for use or disposal. The interleukin-23 agents have vulnerary activity. The method is useful for treating or improving wound healing. This sequence represents a cytokine human interleukin-19 protein used in the wound healing method of the invention.
                                                                                                                                                               Treating inflammatory skin disorders or improving wound healing comprises administering to a subject an agonist or antagonist of Interleukin-23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; interleukin 23; subunit p19; IL-23; IL-23p19; tumour; growth; agonist; rategonist; receptor; cancer; antigon-binding site; antibody; extracellular region; antiense nuoteic acid; small interference RNA; siRNA; polyclonal; monoclonal; humanized; Fab; Fv; F(ab')2; peptide mimetic; colon; ovarian; breast; melanoma; cachexia; anorexia; angiogenesis; gastrointestinal tract; respiratory tract; respiratory tract;
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100.0%; Pred. No. 1.4e-172;
iive 0; Mismatches 0;
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                                 18-DEC-2003; 2003WO-US040937
                                                        23-DEC-2002; 2002US-0436274P
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                                                                                                                                                                                                                                                                                                                                                                            al Similarity 100.
189; Conservative
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                                                                               (SCHE ) SCHERING CORP
                                                                                                                             2004-525781/50.
                                                                                                       Bowman EP, Chen S,
                                                                                                                                        N-PSDB; ADQ14468
                                                                                                                                                                                                                                                                                                                                           Sequence 189 AA;
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         15-JUL-2004.
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Best Local 8
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This sequence represents human interleukin 23 subunit p19 (IL-23p19). The method of the invention for modulating turnour growth comprises contacting a tumour cell with an agonist or antagonist is a binding composition which specifically binds the IL-23 catagonist is a binding composition which specifically binds the IL-23 agonist or antagonist may be used for diagnosing or treating a subject suffering from a cancer or tumour. The binding ormposition comprises an antigen-binding site of the antibody, an extracellular region of IL-23R, antigen-binding site of the antibody, an extracellular region of IL-23R, (siRNA), or a detectable label. The binding composition comprises a polyclonal antibody a monoclonal antibody, a humanized antibody or its fragment, a Fab. Fv. F(ab') 2 fragment, or a peptide mimetic of an antibody. The tumour cell is a colon, ovarian or breast cancer cell, or melanoma cell. In the treatment method, the antagonist of IL-23 inhibits cancer or tumour is of the gastrointestinal tract, respiratory tract, reproductive system or endocrine system. In diagnosing cancer or tumour, cancer or tumour is of the gastrointestinal tract, respiratory tract, the binding composition comprises a nucleic acid probe or primer that specifically binds or hybridises to human or mouse IL-23p19 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modulating tumor growth, useful for treating a subject suffering from cancer or tumor, comprises contacting a tumor cell with an agonist or
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                                                                                                                   /note= "Mature IL-23p19"
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/note= ".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcclanahan TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-668951/65.
N-PSDB; ADS73600.
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Best Local Similarity
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The present invention relates to a method of treating a human subject experiencing a physiological disorder. The method involves administering an agonist or antagonist of DNAX cytokine receptor subunit 5 (DCRS5, also known as IL-23R) or of pl9, where the disorder comprises asthma or allergy, chronic obstructive pulmonary disorder (COPD) or an interstitial lung disorder. The invention is useful for treating interstitial lung disorder e.g. idiopathic pulmonary fibrosis, eosinophilic granuloma and hypersensitivity pneumonitis. The present sequence is the human pl9
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121 VAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVF 180
                                                                                                                                                                                                                                                                                                                                                               Diagnosis; therapeutic; asthma; antiasthmatic; immune disorder;
hilfammation; respiratory disease; allergy; antiallergic;
chronic obstructive pulmonary disease; respiratory-gen.;
pulmonary fibrosis; antiinflammatory; pneumonia; infection; p19 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of an agonist or antagonist of DNAX cytokine receptor subunit 5 (DCRSS) or of p19 for treating a human subject experiencing a physiological disorder such as allergy or chronic obstructive pulmonary disorder (COPD).
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100.0%; Pred. No. 1.4e-172;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moore KW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 6; 89pp; English.
                                                                                                                                                                                          AEA51094 standard; protein; 189 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-NOV-2004; 2004WO-US038886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-NOV-2003; 2003US-00720026
                                                                                                                                                                                                                                                                               11-AUG-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chirica M, Kastelein RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similaricy .vv. Matches 189; Conservative
                                                                                189
                                        181 AHGAATLSP 189
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                                                                                  AHGAATLSP
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                                                                                                                                                                                                                                                                                                                     Human p19 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2005052157-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUN-2005.
                                                                                                                                                                                                                                     AEA51094;
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AEA51094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of detecting (MI) a polynucleotide, by contacting a polynucleotide with a probe (PB) that hybridizes, under stringent wash conditions to at least 394 or 25 contiguous nucleotides of open reading frame of a fully defined interleukin (IL)-B30 sequence of 570 (S1) or 1203 (S2) base pairs, to form duplex, where detection of duplex indicates presence of polynucleotide. The method is useful for detecting IL-B30 polynucleotide, and for detecting levels of IL-B30 polynucleotide, and for detecting levels of IL-B30 in samples from patient suspected of having abnormal conditions such as inflammatory or autoimmune. The method is also useful in forensic science, e.g. to distinguish rodent from human or to distinguish between different cell exhibiting differential expression or modification content of associated with abnormal expression or signaling by IL-B30. This sequence corresponds to the novel interleukin-B30 protein.
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                                                                                                                                                DNA purification; cytokine; interleukin-B30; IL-B30; inflammation; autoimmune disorder; forensic science; differential expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting interleukin-B30 polynucleotide, comprises contacting polynucleotide with probe capable of hybridizing with contiguous nucleotide of polynucleotide to form duplex, where detection of indicates presence of polynucleotide.
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                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                      1. .21
/note= "signal peptide"
22. .189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2; 32pp; English.
                                                                                                        Novel human interleukin B30 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0053765P.
98US-00122443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-2000; 2000US-00558474
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                                                              (first entry)
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Matches 189; Conservative
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                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUL-1997;
24-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                     US6835825-B1
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                                                              10-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                             28-DEC-2004
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                 ADV98151;
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The invention relates to a novel method for treating or improving wound healing. The method comprises administering to a subject an agonist or antagonist of interleukin (IL)-23. The invention further comprises: an agonist of IL-23 derived from the binding site of an antibody that specifically binds to an IL-23 receptor; and a kit comprising the agonist and a compartment or instructions for use or disposal. The interleukin-23 agents have vulnerary activity. The method is useful for treating or improving wound healing. This sequence represents a hyperkine protein used in the wound healing method of the invention.
Treating inflammatory skin disorders or improving wound healing comprises administering to a subject an agonist or antagonist of Interleukin-23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352 RAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHWDLREEGDEETTNDVPHIQCGDGCDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                           agonist; antagonist; interleukin-23; IL-23; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
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                                                                                                                                                                                                                                                 ADQ14473 standard; protein; 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytokine; human; hyperkine
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                                                                                                                                                                                                                                                                                                                                                                                                Human hyperkine protein.
                                                                            181 AHGAATLSP 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bowman EP, Chen S,
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Best Local Similarity
Matches 170; Conserv
                                                                                                                          181 AHGAATLSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                             healing;
                                                                                                                                                                                                                                                                                                                                               07-0CT-2004
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                                                                                                                                                                                                                                                                                                  ADQ14473;
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                                                                                                                                                                                                 RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to recombinant polynucleotide encoding an antiganic interleukin-B30 (IL-B30). The polynucleotides are useful for detecting, isolating, or identifying a DNA clone encoding IL-B30 e.g. from a natural source, particularly for isolating a gene from mammal. The proteins are useful for generating antibodies and for screening drugs. The invention is also useful for diagnostic applications for IL-B30 mediated conditions such as inflammatory conditions and for cell differentiation. The invention is also useful in gene therapy. The present sequence is the human ILB-30 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated or recombinant polynucleotide encoding an antigenic interleukin-B30 (IL-B30), useful in diagnostic applications for IL-B30 mediated conditions such as inflammatory conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22. 189
/note= "Mature human interleukin-30 (IL-B30) protein"
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                                                                                                                                                                                                                                                                                                                                                                                             IL; interleukin; cell differentiation; diagnostic; gene therapy;
drug screening; inflammation; antiinflammatory.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                               Human interleukin-B30 (IL-B30) protein, SEQ ID NO:
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0; Mismatches
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/label= Signal_peptide
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                                                                                                                                                                                                 AEB47331 standard; protein; 189 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-DEC-2004; 2004US-00006154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Matches 189;
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412 QGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSPVAQLHASLLGLSQLLQPEG 471

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This sequence represents human interleukin 23 (IL-23) hyperkine. The method of the invention for modulating tumour growth comprises contacting a tumour cell with an agonist or antagonist of IL-23. The agonist or antagonist is a binding composition which specifically binds the IL-23 p19 subunit (IL-23p19) or the interleukin 23 receptor (IL-23R) protein. The identified agonist or antagonist may be used for diagnosing or treating a subject suffering from a cancer or tumour. The binding or treating a subject suffering from a cancer or tumour. The binding composition comprises an antigen-binding site of the antibody, an extracellular region of IL-23R, a small molecule, an antisense nucleic acid or small interference RNA (sirkNa), or a detectable label. The binding composition comprises a polyclonal antibody, a monoclonal cantibody, a humanized antibody or its fragment, or a peptide mimetic of an antibody. The tumour cell is a colon, ovarian or breast cancer cell, or melanoma cell. In the treatment cachexia, anorexia or angiogenesis. The cancer or tumour, is of the gastrointestinal tract, respiratory tract, reproductive system or cachexia, anorexia or angiogenesis. The cancer or tumour is of the endocrine system. In diagnosing cancer or tumour, the binding composition comprises a nucleic acid probe or primer that specifically binds or hybridises to human or mouse IL-23p19 cDNA sequences, or the human IL-23R
                                                                                                                                                                                                                 agonist, antagonist, receptor, cancer, antigen-binding site, antibody, extracellular region, antisense nucleic acid, small interference RNA, siRNA; polyclonal, monoclonal, humanized, Fab, Fv; F(ab')2, peptide mimetic, colon, ovarian, breast, melanoma; cachexia, anorexia, angiogenesis, gastrointestinal tract, respiratory tract; reproductive system, endocrine system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth, useful for treating a subject suffering from comprises contacting a tumor cell with an agonist or
                                                                                                                                                                                               human; interleukin 23; subunit p19; IL-23; IL-23p19; tumour; growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 89.9%; Score 170; DB 8; Length 52. Best Local Similarity 100.0%; Pred. No. 5.8e-154; Matches 170; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 11; 57pp; English
                  ADS73607 standard; protein; 521 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAR-2004; 2004WO-US007198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-2003; 2003US-0453672P
                                                                                                          (first entry)
                                                                                                                                                   Human IL-23 hyperkine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modulating tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer or tumor,
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                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                        16-DEC-2004
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ADS73607
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to AXY94980, isolated from human adult brain, adult thyroid, adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney, adult placenta, adult tessis, whole embryo, adult cartilage, kidney, foetal brain, adult thymus, foetal placenta, adult tucrus, adult tumour, adult placenta, the polynuclectides adult tumour, adult bladder, cDNA libraries The polynuclectides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or amellorating medical conditions in humans and animals. The polynuclectides can be used as markers for tissues in which the protein is preferentially expressed, as molecular weight markers on Southern gels, and as chromosome markers or tags to identify chromosomes or to map gene positions. The proteins can be used in the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA16618 to AAA16697 encode the human secreted proteins given in AAY94898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides encoding secreted proteins, which may have e.g. untritional, chemokine, immune stimulating or suppressing, hematopoiesis regulating, tissue growth, activin/inhibin antiinflammatory or tumor inhibition activity.
                                                                                                                                                                                                                                                                       Human; secreted protein; immunestimulant; immunesuppressant; virucide; antibacterial; antifungal; cytostatic; antiinflammatory; dermatological; antidasthmatic; antiarthratic; antirheumatic; protozoacide; antithyroid; immune deficiency; severe combined immunedeficiency; SCID; infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus; connective tissue disease; multiple sclerosis; erythematosis; rheumatoid arthritis; autoimmune pulmonary inflammation; asthma; duillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis; insulin dependent diabetes mellitus; graft-versus-host-disease; autoimmune inflammatory eye disease; allergy.
                                                                                                                                                                                                                                      Human secreted protein clone rk80_3 protein sequence SEQ ID NO:138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collins-Racie LA, Evans C;
Steininger RJ, Spaulding V;
 HHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVFAHGAATLSP 189

    Lavallie ER, C
M, Agostino MJ,
Fechtel K;

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                                                                                                                             AAY94966 standard; protein; 189 AA.
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990S-0119931P.
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98US-0099229P.
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                                                                                                                                                                                                    16-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jacobs K, Mccoy JM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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RAVPGGSSPAWTQCQQLSQXLCTLAWSAHPLVGHMDLREEGDEETTNDVPHIQCGDGCDP 352 RAVPGGSSPAWTQCQQLSQXLCTLAWSAHPLVGHMDLREEGDEETTNDVPHIQCGDGCDP

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Search completed: June 20, 2006, 04:52:09 Job time : 145.345 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein

June 20, 2006, 04:52:34 ; Search time 24.5455 Seconds Run on:

(without alignments)
740.869 Million cell updates/sec

US-10-797-157-2 189 1 MLGSRAVWLLLLLPWTAQGR......QAFVAVARVFAHGAATLSP 189 Perfect score:

Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283416 segs, 96216763 residues Searched:

Н Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

pir1:* pir2:* pir3:* PIR 80:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query	Length	DB	ΙD	Description
-1	8	4.2	232	7	G82842	DNA repair protein
7	æ	4.2	299	~	T29226	hypothetical prote
m	80	4.2	313	~	A82640	
4	80	•	391	7	T40169	
Z,	7	3.7	136	~	B95333	
9	7	3.7	151	~	AB1275	
7	7	3.7	151	~	AB1638	
œ	7	3.7	164	~	S18038	u
თ	7	3.7	189	Н	LPHUD	apolipoprotein D p
10	7	3.7	192	~	AE0043	probable membrane
11	7	3.7	209	7	D86758	orotate phosphorib
12	7	3.7	214	~	A83416	hypothetical prote
13	7	3.7	235	~	A99603	
14	7	3.7	238	~	A72374	
15	7	•	248	~	T44932	3-oxoacyl-[acyl-ca
16	7	3.7	254	~	JQ0490	regulatory protein
17.	7	3.7	260	~	F82120	zinc ABC transport
18	7	٠.	273	ч	EDBE12	immediate-early pr
19	7	3.7	284	~	T42608	immediate-early pr
20	7	•	307	7	C70952	probable sugA prot
21	7	3.7	333	~	A96829 .	probable RING fing
22	7	3.7	339	ч	KHIMSB	cathepsin B (EC 3.
23	. 7	٠	339	Н	KHRTB	cathepsin B (EC 3.
24	7	3.7	349	N	T42965	glycoprotein - ate
25	7	•	376	N	B41870	DNA-directed DNA p
56	7	3.7	391	N	T24813	hypothetical prote
27	7	•	393	н	A48573	calreticulin autoa
28	7	3.7	396	N	B70394	
29	7	3.7	413	7	T49545	hypothetical prote

hypothetical prote hypothetical prote	. α	glutamyl-tRNAGIn a	nypornerical proce lysine-tRNA ligase	hypothetical prote	urocanate hydratas	two-component sens	methylmalonyl-CoA	hypothetical C2H2	membrane protein S	carcinoembryonic a	conserved hypothet	hypothetical prote
A99242	H72771	C89978	T2/128 C72221	F83015	S29246	AE1874	A87134	T39291	S55593	A36319	D82825	B71009
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ALIGNMENTS

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DNA repair protein XF0148 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Date: 18-Aug-3000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accesslanc: 83242
C;Accesslanc: 83242
C;Accesslanc: 82512
C;Accesslanc: 82512
C;Accesslance of the plant pathogen Xylella fastidiosa
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Accession: G82842

A Status: preliminary A, Molecule type: DNA A, Residues: 1-232 <SIM>

A; residences: UNDRARC: UPI0000165A4C; GB:AE00386B; GB:AE003849; NID:g9104930; PIDN A; residental source: strain 9a5c

A; Experimental source: strain 9a5c

B; Simpson, A.JG.; Reinard, F.C.; Arruda, P.; Abreug, F.A.; Acencio, M.; Alvarenga, R.; Fineson, A.JG.; Reinard, P.C.; Arruda, P.; Camargo, L.E.A.; Carraro, D.M.; Carrer.; as-Neto, E.; Decena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigrended, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Mattins, E.M.F.; Mattins, E.M.F.; Mattins, B.M.F.; Mattins, B.M.F.; Mattins, A.Y.; Martins, P.; Mattins, B.M.F.; Mattins, D.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.; Rodrigues, V.; Rosa, A.J., de M., de Rosa Jr., V.E.; de Salva, Salva, Salva, Salva, A.C.R.; da Silva, F.R.; Salva, A.C., N., Silva, T., W.A.; da Silva, A.N.; Silva, D.; Vettore, A.L.; N. M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;

A;Reference number: A59328 A;Contents: annotation

C, Genetics

A, Gene: XF0148 C, Superfamily: DNA repair protein radc

Length 232; 4.2%; Score 8; DB 2; 100.0%; Pred. No. 6.5; tive 0; Mismatches Query Match Best Local Similarity 100. Matches 8, Conservative

0; Indels

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Gaps

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181 AHGAATLS 188 |||||||||| AHGAATLS 33 56 δ 셤

RESULT 2

T29226

hypothetical protein F55G1.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T29226 R;Murray, J.; Le, T.T. submitted to the EMBL Data Library, May 1996

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H.; Duesterhoeft,

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114 SLLPDSPV 121
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                                                                                                                                                                                                                                                                                                                                       A; Gene: SPDB:SPBC30B4.03c
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18 AVMLLLL 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 8; Conserv
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                                                                                                                                                                                                                                                                                                      C;Genetics:
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Matches
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    ASIRA
    A,Residues: 1.313 <col>
        ASIRA
    A,Cross-references: UNIPROT:Q9PCLO; UNIPARC:UPIO0000C2819; GB:AE003999; GB:AE003849; NID
    A,Experimental source: strain 95cs.
    Bridones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. S.; Bueno, M.R.P.; Rerincan, A.P.; Ferreira, A.J.S.
    Bublones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. S. Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
    Bublones, M.C.A.; Ferro, J.A.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junquelra, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr Chado, M.A.; Madeira, H.M.F.; Martino, E.M.Y.; Martino, E.A.; Martino, E.M.F.; Mateukuma, A.Y.; Markino, C.L.; Marques, M.V.; Martino, E.A.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Rosa Jr., V.E.; de Oliveira, R.C.; Palmieri, D.A.; Alauthors: da Silva, A.C.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvaira, A.C.; A. Reference number: A59328
    A,Reference number: A59328

A; Description: The sequence of C. elegans cosmid F55G1.

A; Reference number: 220591

A; Accession: T2926

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Residues: 1-299 < MUR>

A; Residues: 1-299 < MUR>

A; Residues: 1-299 < MUR>

A; Residues: 1-290 < MUR>

A; Experimental source: strain Bristol N2; clone F55G1

C; Genetics: A; Experimental source: strain Bristol N2; clone F55G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription regulator LygR family XF1768 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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hypothetical protein SPBC30B4.03c - fission yeast (Schizosaccharomyces pombe)
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.2%; Score 8; DB 2; Best Local Similarity 100.0%; Pred. No. 8.1; Matches 8; Conservative 0; Mismatches
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100.0%; Pred. No. 8.4;
tive 0; Mismatches
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A;Map posttion: 1
A;Introns: 37/1; 121/3
C;Superfamily: pyrroline-5-carboxylate reductase
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Matches 8; Conservative
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hypothetical protein SMa1053 [imported] - Sinorhizobium meliloti (strain 1021) magaplasm C;Species: Sinorhizobium meliloti
C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: B95333
C;Accession: B95333
F;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows: F;Ralman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Accession: B95333
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A;Golecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-136 <KUR>
A;Crose-references: UNIPROT:092ZC0; UNIPARC:UPI00000CB12D; GB:AE006469; PIDN:AAK65228.1;
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
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Cispecies

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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-391 <LYN>
A,Residues: 1-391 <LYN>
A,Cross-references: UNIPROT:074364; UNIPARC:UPI0000698E3; EMBL:AL031262; PIDN:CAA20316.
A,Experimental source: strain 972h-; cosmid c30B4
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R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Hilbert,
submitted to the EMBL Data Library, August 1998
A;Reference number: Z21909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.2%; Score 8; DB 2;
100.0%; Pred. No. 10;
:ive 0; Mismatches
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100.0%; Pred. No. 38;
ive 0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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A,Cross-references: GDB:119690; OMIM:107740
A,Map position: 3q27-3qter
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          A; Residues: 50-74 < KON>
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$18038
homeotic protein S8 - mouse (fragment)
$c;Species: Mus musculus (house mouse)
$c;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Oct-2004
$c;Species: Mus musculus (house mouse)
$c;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Oct-2004
$c;Species: Mus musculus (south) $c;Su0338
$c;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Oct-2004
$c;Species: Date: Nogels, R.; Robert, B.; Kalkhoven, E.; Zwartkruis, F.; de Laaf, L.; E
$A;Accession: 140410
$A;Accession: 140410
$A;Accession: 140410
$A;Status: preliminary; translated from GB/EMBL/DDBJ.
$A;Accession: 140410
$A;Status: preliminary; translated from GB/EMBL/DDBJ.
$A;Accession: 114040
$A;Status: preliminary; translated from GB/EMBL/DDBJ.
$A;Accession: 1-12134, 1988
$A;Cross-references: UNIPROT:Q06348; UNIPARC:UPI000017A2BC; EMBL:X52875; NID:g51365; PID: R;Kongsuwan, K.; Webb, E.; Housiaux, P.; Adams, J.M.
EMBO J. 7, 2131-2138, 1988
$A;Title: Expression of multiple homeobox genes within diverse mammalian haemopoietic lin A;Reference number: $80987; MUID:88329001; PMID:2901346
$A;Accession: $80990
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AB1638
hypotherical protein homolog lin1643 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
G;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB1638
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Sclater 294, 4849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1638
A;Accession: Ab1638
A;Residues: 1-151 <GLA>
A;Cross-references: UNIPROT:Q92BA7; UNIPARC:UP100000CC5FF; GB:AL592022; FIDN:CAC96874.1;
A;AGenetics:
A;Genetics:
A;Genetics: A;Glaser
A; Title: Comparative genomics of Listeria species.

A; Reference number: AB1077; MUD:21537279; PMID:11679669

A; Reference number: AB1077; MUD:21537279; PMID:11679669

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-151 <GLA>

A; Residues: 1-151 <GLA>

A; Cross-references: UNIPROT: Q8Y671; UNIPARC: UP10000055247; GB:NC_003210; PIDN: CAC99680.1

C; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: Genetics: Ge
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Best Local Similarity 100.
Matches 7; Conservative
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A;Title: Human apolipoprotein D gene: gene sequence, chromosome localization, and homolc
A;Reference number: A26958; MUID:87246069; PMID:2439269
A;Accession: A26958
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A; Residues: 1-189 < DRA1>
A; Residues: 1-189 < DRA1>
A; Residues: 1-189 < DRA1>
A; Crose-references: UNIPROT: POS090; UNIPARC: UPI00000369E0; GB: M16648; GB: M16649; GB: M166
A; Crose-references: UNIPROT: POS090; UNIPARC: UPI00000369E0; G: Chen, E.; Comstock, L.; He
J. Biol. Chem. 261, 16535-16539, 1986
A; Title: Cloning and expression of human apolipoprotein D CDNA.
A; Reference number: A03224; MUID: 87057347; PMID: 3453108
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A; Residues: 1-189 < LDRA2.
A; Residues: 1-189 < LDRA2.
A; Cross-references: UNIPARC: UPI00000369E0; GB: J02611; NID: g178840; PIDN: AAB59517.1; PID
A; Note: part of the sequence was confirmed by protein sequencing
R; Balbin, M.; Freije, J.M.P.; Fueyo, A.; Sanchez, L.M.; Lopez-Otin, C.
Biochem. J. 271, 803-807, 1990
A; Title: Apolipoprotein D is the major protein component in cyst fluid from women with h
A; Reference number: S13050; MUID: 91058519; PMID: 2244881
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A; Experimental source: mammary cyst fluid
A; Note: carbohydrate binding sites determined; the sequence of the amino-terminal pyrogl R; Pettsch, M.C.; Boguski, M.E.; Gaskell, S.J.; Yang, M.; Massey, J.B.; Gotto J; R; Yang, C.X.; Gu, Z.W.; Blanco-Vaca, F.; Gaskell, S.J.; Yang, M.; Massey, J.B.; Gotto J; Bjochemistry 33, 1241-12455, 1994

A; Contents: annotation; confirmation of peptide sequence overlap; disulfide bonds; N-gly R; Schindler, P.A.; Settineri, C.A.; Collet, X.; Fielding, C.J.; Burlingame, A.L.
Protean Site-specific detection and structural characterization of the glycosylation of A; Title: Site-specific detection and structural characterization of the glycosylation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Contents: annotation, N-glycosylation
C; Comment: ApoD occurs in the macromolecular complex with lecithin-cholesterol acyltrane
C; Comment: ApoD is primarily localized in HDL (60-65%), with most of the remainder in VI
C; Comment: ApoD has been found in liver, intestine, pancreas, kidney, placenta, adrenal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: apoD; gross cystic disease fluid protein 24 (GCDFP-24) C;Species: Homo sapiens (man) C;Date: 30-Jun-1987 #sequence revision 30-Jun-1987 #text_change 09-Jul-2004 C;Accession: A26958; A03224; $13050 R;brayna, D.T.; McLean, J.W.; Wion, K.L.; Trent, J.M.; Drabkin, H.A.; Lawn, R.M. DNA 6, 199-204, 1987
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                                                                                                             A; Gene: S8
C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;16-72/Domain: homeobox homology <HOX>
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0
                                                                                                                                                                                                                                                                                             Length 164;
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A;Reference number: A57914; MUID:95338133; PMID:7613477
A,Cross-references: UNIPARC:UPI000017A2BD; EMBL:X14572 C;Genetics:
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100.0%; Pred. No. 45;
tive 0; Mismatches
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Best Local Similarity 10v...
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C;Accession: A83416
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q912SO; UNIPARC:UPI00000C54B5; GB:AE004609; GB:AE004091; NID C;Genetics:
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R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUD:21267165; PMID:11353084
A;Accession: A99603
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q98PJ3; UNIPARC:UPI00000C80FF; GB:AL445566; PID:g14090144; P
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                                                                                                                                                                                                                                                                                              hypothetical protein PA1825 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                   C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
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hypothetical protein TM0465 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: A72374
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100.0%; Pred. No. 57;
cive 0; Mismatches
   Pred. No. 55; ; Mismatches
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100.0%; Pred. No. 61;
ive 0; Mismatches
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   100.08;
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Best Local Similarity luv...
7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
                                  Conservative
                                                                                       149 SLSPSQP 155
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   Best Local Similarity
Matches 7; Conserv
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A;Residues: 1-235 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
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A;Genetic code: SGC3
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A;Gene: PA1825
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                  A,Note: the first intron occurs before the initiator codon
C,Superfamily: lipocalin; lipocalin homology
C,Superfamily: lipocalin; lipocalin homology
C,Superfamily: lipocalin; lipocalin homology
C,Superfamily: lipocalin; lipocalin binding; lipid transport; lipoprotein; plasma; pyrogluta
F,12-10/Domain: signal sequence #status experimental <MAT>
F,31-189/Product: apolipoprotein D #status experimental <MAT>
F,37-185/Domain: lipocalin homology <LIP>
F,37-185/Domain: lipocalin homology <LIP>
F,28-134, 61-185/Disulfide bonds: #status experimental
F,58-134, 61-185/Disulfide bonds: #status experimental
F,55,98/Binding site: carbohydrate (Asn) (covalent) #status experimental
F,136/Disulfide bonds: interchain (to apolipoprotein A-II 29) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AE0043

Probable membrane protein YP00349 [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C;Accession: AE0043

R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davie, P.; Dougan, G.; Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q8ZIY5; UNIPARC:UP100000CD6AC; GB:AL590842; PIDN:CAC89208.1;
Genetics YP00349
C;Superfamily: Escherichia coli hypothetical protein b4140
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C;Superfamily: orotate phosphoribosyltransferase; orotate phosphoribosyltransferase homc
C;Keywords: glycosyltransferase; pentosyltransferase
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De6758

Droctate phosphoribosyltransferase (EC 2.4.2.10) [imported] - Lactococcus lactis subsp. C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86758
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis sh;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: D86758
A;Accession: D86758
A;Accession: D86758
A;Accession: D86758
A;Accession: D86758
A;Residues: 1-209 <STO>
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C;Genetics:
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iive 0; Mismatches
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A; Introns: 41/3; 82/2; 112/1
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-192 < KUR>
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Nature 399, 323-329, 1999

A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A,Teference number: A72200; MUID:99287316; PMID:10360571

A,Status: preliminary
A,Status: preliminary
A,Status: DNA
A,Residues: 1-238 <ARN>
A,Cross-references: UNIPROT:Q9WYT6; UNIPARC:UPI0000C1415; GB:AE001724; GB:AE000512; NIC
C,Genetics: C,Genetics: atrain MSB8
C,Genetics: A,Gene: TM0465
C,Superfamily: Thermotoga maritima hypothetical protein TM0465
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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3-oxoacyl-[acyl-carrier-protein] reductase (BC 1.1.1.100) [imported] - Agrobacterium tum C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 05-Oct-2004 C; Accession: 744932 S.K.

8; Kim, K.S.; Farrand, S.K.

J. Bacteriol. 178, 3275-3284, 1996
A; Title: Ti plasmid-encoded genes responsible for catabolism of the crown gall opine mar by the plant tumor.
A; Reference number: 222872; MUID: 96236046; PMID: 8655599
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-248 < KIMs
A; Residues: 1-248 < KIMs
A; Residues: 1-248 < KIMs
A; Residues: 1-248 < KIMs
A; Residues: 1-248 < KIMs
A; Residues: 1-248 < KIMs
C; Genetics: A; Genetics: C; Genetics: C; Superfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology C; Keywords: oxidoreductase

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Length 248; 0; Indels

Query Match 3.7%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 64; Matches 7; Conservative 0; Mismatches

132 SQLLQPE 138 |||||||| 201 SQLLQPE 207

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Search completed: June 20, 2006, 04:59:43 Job time : 27.5455 secs

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1 MLGSRAVMLLLLLPWTAQGR.....QAFVAVAARVFAHGAATLSP 189
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Q6LA37_CAVPO
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O9NPF7_HUMAN
O2O586_FELCA
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Match Local Similarity

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121 VAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVF 180

61 61

1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP

MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG

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GATA_BORBR GATA_BORPA QGGPAS_XENLA QGGPAS_XENLA S39A4 WOUSE Q3UZ63_MOUSE Q4R46_CHLLI Q4QAL9_LEIMA Q4Q905_LEIMA Q4Q905_LEIMA Q40905_LEIMA Q4Y928_PLACH Q19U8_G1BZE	ALIGNMENTS PRT; 189 AA.	<u> </u>	i=11114383; DOI=10.1016/S1 Slom B., Timans J.C., Xu Y. Zonin P., Vaisberg E., igner J., Zurawski S., Liu de Waal-Malefyt R., Hannu les IL-12p40 to form a cyt milar as well as distinct	na, ns, ns. on; EA.
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	LT 1 AS HUMAN Q9HZAS_HUMAN	MAR-2001, MAR-2001, FEB-2006, FEB-2006, erleukin e=IL23A; do sapiens aryota; M malia; Eu	(1) MUCLEOTIDE SEQ NUCLEOTIDE SEQ Oppmann B., Le Yu N., Wang J. Liu MR., Gorn Moore K.W., Re Kastelain R.A. "Novel pl9 pro biological act Immunity 13:71	Copyrighted by Distributed under State of State
	RESULT Q9H2A5 ID	OCC OC BENEFIC	R R R R R R R R R R R R R R R R R R R	3000844444444488

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TISSUE-PCR rescued clones;

X TISSUE-PCR rescued clones;

X Staubberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,

X Riausherg R.L., Feligold E.A., Grouse L.H., Derge J.G.,

X Riausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heng L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

N. Hichards S., Worley N.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley N.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Makesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Radiquez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Generation and initial analysis of more than 15,000 full-length human
                                                                                                           1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                  DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP
  Director MGC Project;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          55-JUL-2004, integrated into UniProtKB/TrEMBL.
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GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
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InterPro; IPR010831; IL23A.
InterPro; IPR003573; IL6 MGF_GCSF.
PANTHER; PTHR15947; IL23A; 1.
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07-FEB-2006, entry version 13.
Interleukin 23, alpha subunit p19,
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SEQUENCE 189 AA;
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X Straubborg R. L., Feingold B. A., Grouse L. H., Derge J. G.,

A Straubborg R. L., Feingold B. A., Grouse L. H., Derge J. G.,

X Klausher R. D., Colling F. S., Wagner L., Shemmen C. M., Schuler G. D.,

A Lischul S. F., Zeeberg B., Buetow K. H., Schaefer C. F., Bhat N. K.,

A Diatchenko L., Marusina K., Farmer A. A., Rubin G. M., Hong L.,

Brownstein M. J., Uddin T. B., Toshiyuki S., Carninol P., Prange C.,

Raha S. S., Loquellano N. A., Peters G. J., Abramson R. D., Mullahy S. J.,

Roas S. A., McEwan P. J., McKernan K. J., Malek J. A., Gunaratne P. H.,

N. Villalon D. K., Muzny D. M., Sodergen B. J., Lu X., Gibbs R. A.,

Raha J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

N. Villalon D. K., Muzny D. M., Sodergen B. J., Lu X., Gibbs R. A.,

Raha J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

M. Hakealey R. W., Touchman J. W., Green B. D., Dickson M. C.,

Rodriguez A. C., Grimwood J., Schmutz J., Myers R. M.,

Bukealey R. W., Krzywinski M. I., Skalska U., Smailus D. E.,

Rohnerch A., Schein J. E., Jones S. J. M., Marra M. A.;

"Generation and initial analysis of more than 15,000 full-length human
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo Bapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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100.0%; Pred. No. 1.9e-106;
iive 0; Mismatches 0; Indels
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Director MGC Project;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 189 AA; 20718 MW; 594290F188EC1B9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                      05-JUL-2004, integrated into UniProtKB/TrEMBL
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GO; GO:0005576; C:extracellular region; IEA.

GO; GO:0005125; F:cytokine activity; IEA.

GO; GO:000555; P:immune response; IEA.

InterPro; IPR012351; Cytokine_4_hix.

InterPro; IPR010831; IL53A.

InterPro; IPR03573; IL6_MGF_GCSF.
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Ensembl; ENSG00000110944; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 12.
Interleukin 23, alpha subunit p19;.
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QGNZ80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=IL23A;
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Matches 121;
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                                                                                                                                                                                                                                                          HUMAN
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Length 189; 64.0%; Score 121; DB 2; Li 100.0%; Pred. No. 1.9e-106; Query Match Best Local Similarity

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1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQXLCTLAWSAHPLVGHMDLREEG

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020586;
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SIGNAL
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NULLOCATIONS SEQUENCE.

X TISSUB-PCR rescued clones,

REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Straubberg R.L., Feingold E.A., Groue L.H., Derga J.G.,

X Alausher R.D., Colline F.S., Wagner L. Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heigh F.,

Browstein M.J., Ugdin T.B., Tobhiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley C.M., Scherger B.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterffield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rohererth A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-228975; PubMed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Baton D., Foster J.S., Grimandi C., Gu Q., Hase P.E., Heldens S.,
M. Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R.L., Wattanabe C., Wieand D., Woods K., Xie M.-H.,
Wood W.I., Godowski P.J., Gray A.M.;
The secreted protein discovery initiative (SPDI), a large-scale
T. "The secreted protein discovery initiative (SPDI), a large-scale
T. "The fort to identify novel human secreted and transmembrane proteins: a
Dioinformatics assessment.";
L. Genome Res. 13:2265-2270(2003).
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                                                                                                                                                     61 DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
                                                                                                                                                                                   61 DEETTNDVPHIQCGDCCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                  1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
                                                                             1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2000, integrated into UniProtKB/TrEMBL.
01-0CT-2000, sequence version 1.
07-FBB-2006, entry version 22.
SGRF precursor (IL-23 p19) (Interleukin 23, alpha subunit p19,).
Name=SGRF; Synonyms=IL23A; ORFNames=UNQ2498;
  ;
0; · Indels
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Hirata Y., Kosuge Y.;
"SRF; a novel member of the IL-6/G-CSF family.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 189 AA.
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              Q9NPF7_HUMAN PRELIMINARY;
Q9NPF7;
  Matches 121; Conservative
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61 DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
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Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                Director MGC Project;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 AA; 20730 MW; 51B5C0F188EC1B9F CRC64;
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.0%; Score 121; DB 2; Le 100.0%; Pred. No. 1.9e-106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ensembl; ENSG0000110944; Homo sapiens.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005125; P:cytokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AB030000, BAA93686.1; -; mRNA.
EMBL; AX359081; AA962942.1; -; mRNA.
EMBL; BC065268; AA466568.1; -; mRNA.
EMBL; BC067511; AA467511.1; -; mRNA.
EMBL; BC067512; AA47512.11; -; mRNA.
EMBL; BC067513; AA467512.11; -; mRNA.
EMBL; AB030001; BAA93687.11; -; Genomic_DNA.
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InterPro; IPR010831; IL23A.
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PANTHER; PTHR15947; IL23A; 1.
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                                                                                       NUCLEOTIDE SEQUENCE.
TISSUE=PCR rescued clones;
                                                                                                                                                                                                                                                                       rescued clones;
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Query Match
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Distributed under the Creative Commons Attribution-NoDerivs License
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064FU1.
25-CCT-2004, integrated into UniProtKB/TrEMBL.
25-CCT-2004, entry version 1.
07-FEB-2006, entry version 8.
Interleukin 23 p19 subunit.
Equus caballus (Horse).
Bikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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Musilova P., Kubickova S., Vychodilova-Krenkova L., Kralik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.2%; Score 25; DB 2; Length 193; llarity 100.0%; Pred. No. 4.7e-15; Conservative 0; Mismatches 0; Indels
                                                             Length 185;
                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                            Hirata Y., Kosuge Y.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
         EMBL; DQ195102; ABB01676.1; -; mRNA.
NON TER 185 185
SEQÜENCE 185 AA; 20433 MW; 344A2940AAFB773B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB030002; BAA93688.1; -; Genomic_DNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR01235; Cytokine 4 hlx.
InterPro; IPR01235; Cytokine 4 hlx.
InterPro; IPR01235; ILé MGF GCSF.
PANTHER; PTR15947; IL23A; I.
FRAN; PF00489; IL6; I.
SEQUENCE 193 AA; 21132 MW; 05F280E94810B9E1 CRC64;
                                                           Similarity 100.0%; Score 31; DB 2; Le Similarity 100.0%; Pred. No. 8.7e-21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                01-OCT-2000, integrated into UniProtKB/TrEMBL.
01-OCT-2000, sequence version 1.
07-PEB-2006, entry version 12.
                                                                                                                193 AA.
                                                                                                     67 DVPHIQCGDGCDPQGLRDNSQFCLQRIHQGL 97
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                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                                                                                                  Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                            NCBI_TaxID=9823;
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Q9и2н9;
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                                                             Query Match
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Distributed under the Creative Commons Attribution-NoDerivs License
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05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 8.
Interleukin-23 pl9 subunit.
Name-IL-23 pl9 subunit.
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Hartley;
Shizatovi I., Seya T.;
"Molecular Cloning and functional characterization of guinea pig
Interleukin -23.";
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Matiasovic J., Hubertova D., Rubes J., Horin P.; "Cytogenetic mapping of immunity-related genes in the domestic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 12.7%; Score 24; DB 2; Length 192; Local Similarity 100.0%; Pred. No. 4.2e-14; nes 24; Conservative 0; Mismatches 0; Indels
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10.6%; Score 20; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                   EMBL; AY704416; AAU13947.1; -; Genomic_DNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR010351; Cytokine_4_hlx.
InterPro; IPR010351; IL23A.
InterPro; IPR01083; IL6 MGF_GCSF.
PANTHER; PT0489; IL6; IL.
SEQUENCE 192 AA; 21042 MW; 9898C79BC9E22E4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AB058509; BAD21123.1; -; mRNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR01231; Cytokine_4_hlx.
InterPro; IPR010331; Cytokine_4_hlx.
InterPro; IPR010331; IL23A.
InterPro; IPR03573; IL6 MGF GCSF.
PANTHER; PTHR1594; IL23Ā; I.
SEQUENCE 189 AA; 20808 MW; BE06A3C59955337F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OGLA37 CAVPO PRELIMINARY, PRT;
QGLA37;
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                                                                                                  Anim. Genet. 36:507-510(2005)
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QBOWE2 PERMA
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Matches
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Q9EQ14_MOU
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Nauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soarse M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
A Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Brownstein M.J., Widnin T.B., Tooshiyuki S., Carninci P., Frange C.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X.; Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Schentz D., Dickson M.C.,
Schriutz A.C., Grimwood J., Schmutz J., Myers R.M.,
Schriefield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,
B. Whiting M., Schein J.B., Jones S.J.M., Marra M.A.,
Schein J.B., Jones S.J.M., Marra M.A.,
Schein J.B., Jones S.J.M., Marra M.A.,
Schein J.B., Jones S.J.M., Marra M.A.,
Schein J.B., Jones B.J.M., Marra M.A.,
Schein J.B., Jones J.M., Marra M.A.,
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                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi,
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinee; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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8.5%; Score 16; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tran G., Hodgkinson S.;
"Rattus norvegicus IL-23 mRNA.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 196 AA; 21986 MW; 188FF74BC409A961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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EMBL; BC098907; AAH98907.1; -; mRNA.
Ensembl; ENSRNOG0000003254; Rattus norvegicus.
                                                                                                 01-DEC-2001, integrated into UniProtKB/TrEMBL.
                                  196 AA.
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GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
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InterPro; IPR010831; IL23A.
InterPro; IPR003573; IL6 MGF GCSF.
PANTHER; PTHR15947; IL23A; 1.
                                  PRT;
                                                                                                                             01-DEC-2001, sequence version 1.
07-FEB-2006, entry version 14.
Interleukin 23, alpha subunit p19.
                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=10116;
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                                                                                                                                                                                                                                  Name=1123a;
                               Q91284_RAT
   RAT
Q91Z84
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                                                                      01-UDN-2003, integrated into UniProtKB/TrEMBL.
01-UDN-2003, sequence version 1:
01-UDN-2003, sequence version 7:
10-UDN-2006, entry version 7:
10-UDN-2008, sequence version 7:
10-UDN-2008, sequence version 7:
10-UDN-2008, sequence version 7:
10-UDN-2008, sequence version 7:
10-UDN-2008, sequence version 7:
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10-UDN-2008, sequence version 7:
10-UDN-2008, sequence version 7:
10-UDN-2008, sequence version 7:
10-UDN-2008, sequence version 7:
10-UDN-2008, sequence version 7:
10-UDN-2008, sequence version 7:
10-UDN-2008, sequence version 7:
10-UDN-2008, sequence version 7:
10-UDN-2008, sequence 
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MEDLINE=20567322; PubMed=11114383; DOI=10.1016/S1074-7613(00)00070-4;
MEDLINE=20567322; PubMed=11114383; DOI=10.1016/S1074-7613(00)00070-4;
Oppmann B., Leeley R., Blom B., Timans J.C., Xu Y., Hunte B., Vega F.,
Yu N., Wang J., Singh K., Zonin F., Vaisberg E., Churakova T.,
Liu M.-R., Gorman D., Wagner J., Zurawski S., Liu Y.-J., Abrams J.S.,
Mooree K.W., Rennick D., de Waal-Malefyt R., Hannum C., Bazan J.F.,
Kastelein R.A.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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01-MAR-2001, sequence version 1.
07-FBB-2006, entry version 2.
Interleukin 23, alpha subunit (Interleukin 23, alpha subunit p19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.4%; Score 14; DB 2; Length 184
100.0%; Pred. No. 0.00013;
Ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schountz T.; "Cloning of deer mouse interleukin-23a p19 subunit."; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AY259629; AAP15041.1; -; mRNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005125; F:eytokine activity; IEA.
GO; GO:0006955; F:eytokine ectivity; IEA.
InterPro; IPR012351; Cytokine 4 hlx.
InterPro; IPR010331; IL23A.
InterPro; IPR001573; IL6 MGF-GCSF.
PANTHER; PTHR1947; IL23A; I.
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    184 AA
    PRT;
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100.0%; Pre-
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 DNSQFCLQRIHQGL 97
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NUCLEOTIDE SEQUENCE.
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Gaps ö

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Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                initiative.
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STRAIN=FVB/N; TISSUE=Mammary tumor. C3;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A platchenko L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schuutz J., Myers R.M.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

A moving Chan and initial analysis of more than 15,000 full-length human
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Distributed under the Creative Commons Attribution-NoDerivs License
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1-FEB-2006, entry version 2.

Hypothetical protein.

Xenopus laevis (African clawed frog).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Amphibia; Batrachia, Anura, Mesobatrachia; Pipoidea, Pipidae;

Xenopodinae, Xenopus, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22341132, PubMed=12454917, DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.3%; Score 12; DB 2; Length 196;
100.0%; Pred. No. 0.011;
ve 0; Mismatches 0; Indels
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SEQUENCE 196 AA; 22071 MW; DAF4A318A2DD3B7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF301619; AAG37231.1; -; MRNA.
EMBL; BC019953; AAH19953.1; -; MRNA.
Ensembl; BNSUSG000000025383; Mus musculus.
MG1: 1932410; 1123a.
GO; GO:0005615; C:extracellular space; RCA.
InterPro; IPR012531; Cytckine 4 hlx.
InterPro; IPR012531; ILG3A.
InterPro; IPR003573; ILG MGF GCSF.
InterPro; IPR003573; ILG MGF GCSF.
PANTHER; PTHR15947; ILC3A; ILC3A; ILG; PF00489; ILG2A; ILC3A; ILG2A; ILG2A; ILG2A; ILG2A; ILG2A; ILG2A; ILG2A; ILG3A; I
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NIH MGC Project;
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Q4V817;
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nes 12; Conservative
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OGV0817 XEN
DO Q4V81
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DT 05-JU
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.R., Bhat N.K.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.R., Bhat N.K.,
Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McZwan P.J., McKernan R.J., Malke J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villaton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Redeneration and initial analysis of more than 15,000 full-length human
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PubMed=15980861; DOI=10.1038/nbbill100.
Paulsen I.T., Press C.M., Ravel J., Kobayashi D.Y., Myers G.S.A., Mauyed I.T., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J., Durkin A.S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.J., Gwinn M.L., Schneider D.J., Cartinhour S.W., Nelson W.C., Weldman J., Watkins K., Tran K., Khouri H., Pierson E.A., Complete genome sequence of the plant commensal Pseudomonas fluorescens Pf-5."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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OrderedLocusNames=PFL 0640;
Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477).
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales;
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0
                                                                                                                       TISSUE=0vary;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IISSUE=Ovary;
Klein S., Gerhard D.S.;
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databaees.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 151 AA; 17574 MW; 4CAD3E036FF461B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC097607; AAH97607.1; -; mRNA.
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Dev. Dyn. 225:384-391(2002).
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                                                                                      NUCLEOTIDE SEQUENCE
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21 AVPGGSSP 28
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                                                                         NCBI_TaxID=99883;
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                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "An integrated gene annotation and transcriptional profiling approach towards the full gene content of the Drosophila genome."; Genome Biol. 5.RESEARCH0003.1.FESEARCH0003.1.7(2003).
-!- MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-2005, integrated into UniProtKB/TrEMBL.
19-JUL-2006, sequence version 1.
07-FEB-2006, entry version 3.
Chromosome 9 SCAF14729, whole genome shotgun sequence. (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

Bridden (1709175, DOI=10.1186/gb-2003-5-1-r3),

Hild M., Beckmann B., Haas S.A., Koch B., Solovyev V., Busold C.,

Fellenberg K., Boutros M., Vingron M., Sauer F., Hoheisel J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 102;
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                                                                                                                                                                                          Length 538
                                                                                                                                                                                                                   Indele
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SEQUENCE 102 AA; 10874 MW; 87EABD1E1318C175 CRC64;
                                                                                                                                                                  538 AA; 56824 MW; 6976E2EB1BFA58D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004, integrated into UniProtKB/TrEMBL.
05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 8.
                                                                                                                                                                                          DB 2;
                                                            EMBL, CP000076, AAY96047.1; -; Genomic_DNA.
GO; GO:0015020; C:membrane; IEA.
GO: GO:0005488; F:binding; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                    102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.2%; Score 8; DB 2
100.0%; Pred. No. 40;
iive 0; Mismatches
                                                                                                                                                                                                 100.0%; Preα. .....
                                                                                                                                                                                          4.8%; Score 9; I
100.0%; Pred. No.
                                                                                                                        InterPro; IPR001851; Bac inmem transp. Pfam; PF02653; BPD_transp_2; 1.
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Biotechnol. 23:873-878(2005)
                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
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51 LLLLPWTAQ 59
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Best Local Similarity
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QGIM10 DROME
QGIM10;
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"An integrated
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Q4S5NO TETNG
D Q4S5NO, TETNG
AC Q4S5NO;
DT 19-JUL-2005, st
DT 7-FEB-2006, st
DE Chromosome 9 St
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Whede-15496914; DOI=10.1038/nature03025;
Whose-15496914; DOI=10.1038/nature03025;
Waillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Malcaud S., Jaffe D., Fischer C., Lutfalla G., Dossat C., Segurens B., Dasilya C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Anthouard V., Salanoubat M., Levy M., Boulain J., De Berardinis V., A Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Perra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., M. Kellis M., Volff J.-M., Guigo R., Zody M.C., Mestroov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Lindblad-Toh K., Sarathi W., Scarpelli C., Micker P., Lander E.S., Weissenbach J., Roest Crollius H., Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Terraodon nigroviridis (Green puffer).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Meopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FBS-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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100.0%; Pred. No. 49;
ative 0; Mismatches
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Search completed: June 20, 2006, 04:58:47 Job time : 194.945 secs

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1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
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Best Local Similarity 100.
Matches 189; Conservative
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                                                                                                                              1 MLGSRAVMLLLLLPWTAQGR......QAFVAVAARVFAHGAATLSP 189
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Sequence 2,
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                                                              ; Search time 35.8364 Seconds
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd
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US-09-558-089-2
US-09-558-087-2
US-09-935-366A-2
US-09-687-6378-1
US-09-687-6378-24
US-09-687-6378-24
US-09-687-6378-25
US-09-687-6378-25
US-09-687-6378-25
US-09-558-089-5
US-09-935-3664-5
US-09-935-3664-5
US-09-935-368-089-4
US-09-558-089-4
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                                                                                                                                                                                  650591 seqs, 87530628 residues
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                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                        - protein search, using sw model
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                                                              June 20, 2006, 04:59:09
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189
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Match Length
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Perfect score:
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Maximum DB
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Sequence 211, App
Sequence 9703, Ap
Sequence 7690, Ap
Sequence 6, Appli
Sequence 13092, A
Sequence 48309, A
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Sequence 13, Appl
Sequence 6103, Ap
Sequence 2, Appli
Sequence 257, Ap
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1, Appli
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Sequence 20936, R
Sequence 21443, R
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Patent No. 6060284

GENERAL INFORMATION:

PAPLICANT:

PAPLICANT:

MUMBER OF INVENTION:

MAMMALIAN CYTOKINE; RELATED REAGENTS

NUMBER OF SEQUENCES:

ADDRESSE:

ADDRES
                                            US-09-489-039A-9703
US-09-949-016-7690
US-08-505-617-6
US-09-018-170-6
US-09-2700-767-33092
US-09-270-767-48309
US-09-975-456B-10
US-09-975-456B-10
US-09-975-456B-10
US-09-252-991A-20936
US-09-252-991A-20436
US-09-605-703B-1344
US-09-605-703B-1344
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US-09-270-767-46068
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9 9

Gaps

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Length 189; Indels

100.0%; Score 189; DB 2; L 100.0%; Pred. No. 1.8e-167; tive 0; Mismatches 0;

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61 DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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0
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TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 189; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.8e-167;
Matches 189; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: USA

CURTURE READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PACENTIN REAGASE #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/558,087

FILING DATE: 25-Apr-2000

CLASSIFICATION NUMBER: US 60/053,765

FILING DATE: 25-Apr-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REGISTRATION NUMBER: 34,090

REGISTRATION NUMBER: DX0758K1

TELECOMMUTICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
                                                                                                                                                                                                                       Sequence 2, Application US/09558087
Patent No. 6495667
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 189 amino acids TYPE: amino acid
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US-09-558-474-2
'Sequence 2, Application US/09558474
'Patent No. 6835825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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STATE: California
181 AHGAATLSP 189
                                                             181 AHGAATLSP 189
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                                                                                                                                                                                           US-09-558-087-2
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                                                                    DEETTNDVPHIQCGDCCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
                                                                                                                                                                                                  VAQLHASLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVF 180
                              DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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TITLE OF INVENTION: MAMMALIAN CYTOKINE, RELATED REAGENTS
NUMBER OF SEQUENCES: 16
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MEDIUM TYPE: Floppy disk
COMPUTER: Bar Floppy disk
COMPUTER: Law PC compatible
COMPUTER: Date of the post of the po
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ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
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sequence DESCRIPTION: SEQ ID NO: 2:
US-09-558-089-2
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Patent No. 6479634
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 VAQLHASILGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVF 180
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GENERAL INFORMATION:
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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Patent No. RE39015
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAWMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
CORRESPEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDLUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/558,474

FILING DATE: 25-Apr-2000

CLASSIFTCATION: vinknown>

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REGISTRATION INFORMATION:

TELECOWUNINICATION INFORMATION:

TELECOWUNINICATION INFORMATION:

TELECOWUNINICATION INFORMATION:

TELECOWUNINICATION INFORMATION:

TELECOWUNINICATION INFORMATION:

TELECOWUNINICATION INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 1.8e-167;
Matches 189; Conservative .0; Mismatches 0; Indels
                                                                                                                       ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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STATE: California
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US-09-935-366A-2
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COMPUTER: READMAILE PORN:
COMPUTER: IRR PC Compatible
COMPATING SYSTEM: C-DOS/MA-D-OS
SOFTWARE PALCATION MAY.
CURRENT APPLICATION WAS AND STATEMENT OF SYSTEMS
PRIOR MAPLICATION NAME: C-DOS/MAS-D-OS
CURRENT APPLICATION NAME: C-DOS/MAS-D-OS
CURRENT APPLICATION NAME: C-DOS/MAS-D-OS
CURRENT APPLICATION NAME: 0,009/935.366A
ATTORNEY/ARENT INDOMER: 09/122.443
ATTORNEY/ARENT INDOMER: 09/122.443
ATTORNEY/ARENT INDOMER: 09/122.443
ATTORNEY/ARENT INDOMER: 09/122.443
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ATTORNEY/ARENT INDOMER: 09/122.443
ATTORNEY/ARENT INDOMER: 09/122.400
INTORNATION PRESENCE/COCKET WOMER: 09/122.200
INTORNATION PRESENCE/COCKET WOMER: 00/122.200
INTITLE PRESENCE/COCKET WOMER: 00/122.200
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; Sequence 25, Application US/09687637B
; Patent No. 6610285
; GENERAL INFORMATION:
; APPLICANT: Hirada, Yuichi
; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; FILE REFERENCE: 06501-067001
; CURRENT PELLING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/JP99/01997
; PRIOR PELLING DATE: 1999-04-14
; PRIOR PILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PSECSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENTH: 53
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TITLE OP INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
TITLE OP INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
CURRENT APPLICATION NUMBER: US/09/687,637B
CURRENT FILING DATE: 1090-01-013
PRIOR PILING DATE: 1999-04-14
PRIOR FILING DATE: 1999-04-14
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PASICEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 54
                                                                                                                                  1 MLGSRAVMILILILPWTAQGRAVPGGSSPAWTQCQQLSQXLCTLAWSAHPLVGHMDLREEG 60
                                                                                          1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
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      Length 189;
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                                             0; Indels
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Query Match 64.0%; Score 121; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.2e-104;
Matches 121; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
28.0%; Score 53; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 8.6e-42;
Matches 53; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/09687637B; Patent No. 6610285; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rypE: PRT
CORGANISM: Homo sapiens
US-09-687-6378-22
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US-09-687-637B-25
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Gaps

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US-09-687-637B-24
US-09-687-637B-24
Sequence 24, Application US/09687637B
Sequence 24, Application US/09687637B
Sequence 24, Application US/09687637B
Sequence 24, Application US/09687637B
SET INTER OF INVENTION:
TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
FILE REFERENCE: 06501-067001
CURRENT APPLICATION NUMBER: US/09/687,637B
SPRIOR FILING DATE: 1999-04-14
PRIOR FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-607-6378-23
; Sequence 23, Application US/09687637B
; Sequence 23, Application US/09687637B
; Patent No. 661028B
; GENERAL INFORMATION:
; TITLE OF INVENTYON: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; TITLE OF INVENTYON: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; TITLE OF INVENTYON: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; CURRENT APPLICATION NUMBER: DS/00-10-13
; CURRENT FILING DATE: 1299-04-14
; PRIOR FILING DATE: 1999-04-14
; PRIOR FILING DATE: 1999-04-14
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 46
; SCFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; TENGTH: 33
; TENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
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137 PEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVFAHGAATLSP 189
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                           1 PEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAARVFAHGAATLSP
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2e-23;
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18.0%; Score 34; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 3.4e-24;
Matches 34; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 FCLORIHOGLIFYEKLLGSDIFTGEPSLLPDSPV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FCLORIHQGLIFYEKLLGSDIFTGEPSLLPDSPV 34
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17.5%; Score 33; DB
Best Local Similarity 100.0%; Pred. No. 2e-
Matches 33; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Homo Bapiens
US-09-687-637B-24
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NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: (650)852-9196
                                                                                                                          INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09558087
Patent No. 6495667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
                                                                                                            TELEPHONE: (650)852-919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (650) 496-1200
                 ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94304-1104
COMPUTER READABLE FORM:
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Best Local Similarity 100.(
Matches 25; Conservative
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Best Local Similarity
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TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADBRESSE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 102;
Bazan, J. Fernando
/ENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                          COUNTRIE 1994

ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 24-JUL-1998
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Le
1.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 13.2%; Score 25; DB 1 Similarity 100.0%; Pred. No. 1.5 25; Conservative 0; Mismatches
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APPLICATION NUMBER: US/09/558,089
                       APPLICATION NUMBER: 09/122,443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 KILRSLQAFVAVAARVFAHGAATLS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                34,090
PRR: DX0758K1
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,765
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09558089
Patent No. 6479634
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 102 aming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              not relevant
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ching, Edwin P.
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-122-443-5
               TITLE OF INVENTION: MAI
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 25; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-558-089-5
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APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SECUENCES: 16
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/558,087
FILING DATE: 25-Apr-2000
CLASSIFICATION: Unknown>
                                                                                                                                                                                     13.2%; Score 25; DB 2; L6 100.0%; Pred. No. 1.5e-15; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.2%; Score 25; DB 2; Le 100.0%; Pred. No. 1.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,765
FILING DATE: 25-UL-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TYPE: amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: perior
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-558-089-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: not relevant
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-558-087-5
                                                                                                                                                                                                                                                                                  164 KILRSLOAFVAVAARVFAHGAATLS 188
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Gaps
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Patent No. RE39015
GENERAL INPORMATION
GENERAL INPORMATION:
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                          Sequence 5, Application US/09558474
Patent No. 6835825
GENERAL INFORMATION:
APPLICANT: Bazan, J. Fernando
TITLE OF INVENITON: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
COMPUTE: California
COUNTRY: USA
ZUE: 94104-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopyy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRING APPLICATION DATA:
APPLICATION NUMBER: US/09/558,474
FILING DATE: 25-Apr-2000
CLASSIFICATION: vUnknown>
PRIOR APPLICATION NUMBER: US 60/053,765
FILING DATA:
APPLICATION NUMBER: US 60/053,765
FILING DATA:
APPLICATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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  0; Indels
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:

TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-558-474-5
                                              164 KILRSLQAFVAVAARVFAHGAATLS 188
                                                                                   77 KILRSLQAFVAVAARVFAHGAATLS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 KILRSLQAFVAVAARVFAHGAATLS 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.(
Matches 25; Conservative
  25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
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                                                                                                                                                              RESULT 14
US-09-558-474-5
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  Matches
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COMPUTATION

COMPUTATION

COMPUTATION

MEDIUM TYPE: Ploppy disk

MEDIUM TYPE: Floppy disk

COMPUTATION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.30

CURRENT APPLICATION NUMBER: US/09/935,366A

FILING DATE: 2-Aug-2001

CLASSIFICATION NUMBER: 09/122,443

FILING DATE: CUNKnown>

PRIOR PEDICATION NUMBER: 09/122,443

FILING DATE: CUNKnown>

APPLICATION NUMBER: 09/122,443

FILING DATE: CUNKnown>

MANE: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REGISTRATION NUMBER: 34,090

REGISTRATION NUMBER: 34,090

REGISTRATION NUMBER: 34,090

MANE: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

MANE: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

MANE: Ching Cocket NUMBER: 050,052-9196

TELEPHONE: (650) 852-9196

TELEPHONE: (650) 852-9196

TELEPHONE: COSO 10 NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 102 amino acids

TYPE: amino acids

TYPE: amino acid

STANDENNESS: NO: RE39015 Relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

MOLECULE TYPE: 00004; Pered. No. 1.56-15;

MATCHOS 25; CONSERVATION: 00004; Pered. No. 1.56-15;

MATCHOS 25; CONSERVATIVE 00. Mismatches 0; Indels 0; Gaps
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Search completed: June 20, 2006, 05:01:01 Job time: 36.8364 secs

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                                                     June 20, 2006, 04:59:59; Search time 132.055 Seconds (without alignments) 662.966 Million cell updates/sec
                                                                                                                                                                                                                                                                          Published Applications AA Main:*

| FMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| FMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| FMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| FMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
| FMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
| FMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                        189
1 MLGSRAVMLLLLEPWTAQGR......QAFVAVAARVFAHGAATLSP 189
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-956-984-14

US-09-969-984-14

US-10-121-049-232

US-10-121-049-232

US-10-121-904-232

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US-10-176-918-232

US-10-176-918-232

US-10-176-918-232
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                                                                                                                                                                  2097797 segs, 463214858 residues
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                                     - protein search, using sw model
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seq length: 200000000
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Match Length D
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                                      OM protein
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Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	
US-10-143-032-232	US-10-123-108-232	US-10-123-236-232	US-10-123-261-232	US-10-140-921-232	US-10-140-928-232	US-10-121-045-232	US-10-123-292-232	US-10-123-903-232	US-10-124-819-232	US-10-124-822-232	US-10-140-925-232	US-10-160-498-232	US-10-124-824-232	US-10-127-825A-232	US-10-127-829A-232	US-10-127-835A-232	US-10-127-839A-232	
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121	121	121	121	121	121	121	121	121	121	121	121	121	121	121	121	121	121	
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ALIGNMENTS

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DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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Pred. No. 3.8e-163;
; Mismatches 0;
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ORGANISM: Unknown Organism
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Best Local Similarity 100.
Matches 189; Conservative
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181 AHGAATLSP 189
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181 AHGAATLSP 189
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ORGANISM: Homo sapiens
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LENGTH: 189
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Publication No. US20040223969A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: USES OF IL-23 AGONISTS AND ANTAGONISTS; RELATED REAGENTS;
FILE REFERENCE: DX06022USO1
CURRENT APPLICATION NUMBER: US/10/797,157
CURRENT APPLICATION NUMBER: US. 60/453,672
PRIOR APPLICATION NUMBER: US. 60/453,672
PRIOR APPLICATION NUMBER: US. 60/453,672
SPRIOR SEQ ID NOS: 11
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
SEQ ID NO 2
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Publication No. US20040213761A1
GENERAL INFORMATION:
APPLICANT: Bownan, Edward P.
APPLICANT: Chan, Jason R.
APPLICANT: Mouven, Wolven, Tatyana
APPLICANT: Churakova, Tatyana
APPLICANT: Chan, Shi-Juan
APPLICANT: Chan, Shi-Juan
APPLICANT: Chan, Daniel J.
TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
FILE REFERENCE: DX01578K
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Best Local Similarity 100.0%; Pred. No. 3.8e-163;
Matches 189; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/742,405
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 189
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Matches 189; Conservative
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181 AHGAATLSP 189
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
US-10-797-157-2
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US-10-742-405-4
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US-10-797-157-2
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Sequence 6, Application US/10720026;
Publication No. US20040258686A1
GENERAL INFORMATION:
APPLICANT: Chirica Madaline
APPLICANT: Parham, Christi L.
APPLICANT: Ratelein, Robert A.
APPLICANT: Moore, Kevin W.
TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
FILE REFERENCE: DX01074B1K
CURRENT APPLICATION NUMBER: US/10/720,026
CURRENT FILING DATE: 2003-11-21
FRIOR PILING DATE: 2000-05-10
FRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.2
                                                                                                                                                             61 DEETTINDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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1 MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEG
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100.0%; Score 189; DB 5; Length 189;
Best Local Similarity 100.0%; Pred. No. 3.8e-163;
Matches 189; Conservative 0; Mismatches 0; Indels 0
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Publication No. US20050158750A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
STREET: 901 California Avenue
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Sequence 14, Application US/09965528
Publication No. US20020187523A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: TANG, Y. Tom
APPLICANT: TAL, Preeti
APPLICANT: BURFORD, Nell
APPLICANT: BURFORD, Nell
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Olga
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Matches 170; Conservative
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; ORGANISM: Homo sapiens
US-10-797-157-11
SEQ ID NO 8
LENGTH: 521
TYPE: PRT
ORGANISM: Homo sapiens
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Squence 10 No. US20040213761A1

GENERAL INFORMATION:

APPLICANT: Bowman, Edward P.

APPLICANT: Chan, Jason R.

APPLICANT: Chan, Shi-Juan

APPLICANT: Chan

APPLICANT: Chan, Shi-Juan

APPLICANT: Chan, Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/006,154

FILING DATE: 06-Dec-2004

CLASSIFICATION NUMBER: US/09/935,366

FILING DATE: 22-Aug-2001

APPLICATION NUMBER: 09/122,443

FILING DATE: CURNOWN:

ATTORNEY/AGENT INFORMATION:

NAME: CLAING DATE: CURNOWN:

FILING DATE: CURNOWN:

ATTORNEY/AGENT INFORMATION:

NAME: CLAING CANIN P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0758K1

TELEPHONE: (650) 852-9196

NEMERICATION INFORMATION:

TELEPRAK: (650) 852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: procein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-11-006-154-2
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SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
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                                             STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AHGAATLSP 189
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Sequence 11, Application US/10797157

Publication No. US20040223969A1

GENERAL INFORMATION:
APPLICATY: Off. Martin
APPLICATY: McClanahan, Terrill K.
TITLE OF INVENTION:
TITLE OF INVENTION: UNBER: US/10/797,157
CURRENT APPLICATION NUMBER: US/10/797,157
CURRENT PILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: U.S. 60/453,672
PRIOR APPLICATION NUMBER: U.S. 60/453,672
PRIOR APPLICATION NUMBER: U.S. 60/453,672
SPRIOR PILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 11
SSOTUME OF SEQ ID NOS: 11
SSOTUME OF 11.
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                                                                                                                                                                                                                                                  80 QCLRDNSQPCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSPVAQLHASLLGLSQLLQPEG 139
                                                                                                                                                                                                                                                                                                            412 OGLRDNSQFCLORIHOGLIFYEKLLGSDIFTGEPSLLPDSPVAQLHASLLGLSQLLQPEG 471
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                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                              ;
Query Match 89.9%; Score 170; DB 4; Length 521; Best Local Similarity 100.0%; Pred. No. 1.7e-145; Matches 170; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.7e-145;
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US-09-774-046A-138

US-09-774-046A-138

Sequence 138

Publication No. US20030096951A1

GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: ACCO, John M.
APPLICANT: ACCO, John M.
APPLICANT: APELICANT: ACCO, John M.
APPLICANT: Pans, Cheryl
APPLICANT: Preacy, Marice
APPLICANT: Spanishing David
APPLICANT: Spanishing Nikal
APPLICANT: Spanishing Vikki
APPLICANT: Spanishing, Vikki
APPLICANT: Spanishing, Vikki
APPLICANT: Clark, Hilary
APPLICANT: Clark, Hilary
APPLICANT: Grachishing Nikki
APPLICANT: Grachish Kim
APPLICANT: Grachish Kim
APPLICANT: Grachish Kim
APPLICANT: Grachish Kim
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APPLICANT: Grachish Kim
APPLICANT: Grachish Kim
APPLICANT: Grachish Kim
APPLICANT: Grachish Kim
APPLICANT: Grachish Kim
APPLICANT: BREREENCE: GI 6075-83A
CURRENT APPLICATION NUMBER: 1999-08-13
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 138
LENGTH: 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEETTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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100.0%; Pred. No. 2e-101;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020187523A1 2933038CD1
US-09-965-528-14
APPLICANT: AZIMZAI, Yalda
APPLICANT: LU, Dyung Ahna M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
FILE REFERENCE: PF-0710 USA
CURRENT APPLICATION NUMBER: US/09/965,528
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/144,270
PRIOR APPLICATION NUMBER: 60/144,270
PRIOR APPLICATION NUMBER: 60/146,700
PRIOR APPLICATION NUMBER: 60/146,700
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 55
SOOTWARE: PERL PROGRAM
SEQ ID NO 14
LENGTH: 189
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Best Local Similarity 100.
Matches 121; Conservative
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ORGANISM: Homo sapiens
US-09-374-046A-138
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APPLICANT: YUE, Henry
APPLICANT: YUE, Henry
APPLICANT: BURFORD, Neil
APPLICANT: BANDRAN, Olga
APPLICANT: BANDRAN, Olga
APPLICANT: BANDRAN, Olga
APPLICANT: BANDRAN, Olga
APPLICANT: BANDRAN, Olga
APPLICANT: BANDRAN, Olga
APPLICANT: BATTERSON, Chandra
APPLICANT: PATTERSON, Chandra
CURRENT APPLICATION NUMBER: US/09/969,984
CURRENT FILING DATE: 1999-05-19, 1999-07-10, 1999-10-04
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PERL PROGram
SEQ ID NO 14
LENGTH: 189
                                                                                                                                                                                            61 DEETTNDVPHIQCGDGCDPQCLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSP 120
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                                                     Gapa
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  Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040048244A1 2933038CD1
US-09-969-984-14
Query Match 64.0%; Score 121; DB 3; Length 18 Best Local Similarity 100.0%; Pred. No. 2e-101; Matches 121; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09969984 Publication No. US20040048244A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUDLICATION NO. OLSCOWANCESATION,
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: TANG, Y. Tom
APPLICANT: YUE, Henry
APPLICANT: LAL, Preect
APPLICANT: BANDMAN, Olst
APPLICANT: BANDMAN, Olst
APPLICANT: BANDMAN, Olst
APPLICANT: AZIMZAI, Yalda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                121 V 121
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US-10-028-072-232
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FRIOR FILING DATE: 1998-04-09
PRIOR PILING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-14
PRIOR FILING DATE: 1998-04-14
PRIOR PILING DATE: 1998-04-14
PRIOR PILING DATE: 1998-04-14
PRIOR PILING
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R APLLING DATE: 1998-04-29
R APPLICATION NUMBER: 60/084600
R FILING DATE: 1998-05-07
SR APPLICATION NUMBER: 60/084627
TOTAL NUMBER: 60/084627
                                                                     RELING DATE: 1997-10-17
R APPLICATION NUMBER: 60/064248
R FILING DATE: 1997-11-03
R FILING DATE: 1997-11-03
R FILING DATE: 1997-11-03
R APPLICATION NUMBER: 60/065186
R APPLICATION NUMBER: 60/065186
R APPLICATION NUMBER: 60/065846
R FILING DATE: 1997-11-12
R FILING DATE: 1997-11-12
R FILING DATE: 1997-11-24
R FILING DATE: 1997-11-24
R FILING DATE: 1997-11-24
R FILING DATE: 1997-11-24
R APPLICATION NUMBER: 60/066511
R FILING DATE: 1997-11-24
R APPLICATION NUMBER: 60/066512
R FILING DATE: 1997-11-24
R APPLICATION NUMBER: 60/069212
R FILING DATE: 1997-12-11
R APPLICATION NUMBER: 60/069218
R FILING DATE: 1997-12-11
R APPLICATION NUMBER: 60/069218
R FILING DATE: 1997-12-11
R APPLICATION NUMBER: 60/069314
R FILING DATE: 1997-12-11
R APPLICATION NUMBER: 60/069218
R FILING DATE: 1997-12-11
R APPLICATION NUMBER: 60/069218
R FILING DATE: 1997-12-11
R APPLICATION NUMBER: 60/06934
R FILING DATE: 1997-12-11
R APPLICATION NUMBER: 60/06934
R FILING DATE: 1998-10-23
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R FILING DATE: 1998-02-04

R FILING DATE: 1998-02-09

R APPLICATION NUMBER: 60/074086

R APPLICATION NUMBER: 60/074092

R APPLICATION NUMBER: 60/07791

R FILING DATE: 1998-02-09

R PILING DATE: 1998-03-12

R APPLICATION NUMBER: 60/07791

R PILING DATE: 1998-03-20

R APPLICATION NUMBER: 60/078910

R PILING DATE: 1998-03-22

R FILING DATE: 1998-03-22
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FILING DATE: 1998-05-12
APPLICATION NUMBER: 60/085323
FILING DATE: 1998-05-13
                                       PLICATION NUMBER: 60/063755
LING DATE: 1997-10-17
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FILING DATE: 1998-03-27
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FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/081817
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081818
FILING DATE: 1998-04-15
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FILING DATE: 1998-04-24
APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
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FILING DATE: 1998-02-27
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FILING DATE: 1998-05-07
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CURRENT APPLICATION NUMBER: US/10/028,072

CURRENT PELLING DATE: 2001-12-19

PRIOR PELLOATION NUMBER: 60/05914

PRIOR PELLING DATE: 1997-06-18

PRIOR PELLING DATE: 1997-09-17

PRIOR PELLING DATE: 1997-09-19

PRIOR PELLING DATE: 1997-10-17

PRIOR PELLING DATE: 1997-10-17

PRIOR PELLING DATE: 1997-10-17

PRIOR PELLING DATE: 1997-10-24

PRIOR PELLING DATE: 1997-10-27

PRIOR PELLING DATE: 1997-10-29

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APPLICATION UNDBER: 60/03735
FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063738
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                                                                              Desnoyers, Luc
Filvaroff, Ellen
Gao, Wel-Qiang
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Goddard, Audrey
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Watanabe, Colin K
Wood, William
Beresini, Maureen
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Gurney, Austin
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R181: US/10/140,808
CURRENT APPLICATION NUMBER: US/10/140,808
CURRENT FILING DATE: 2002-05-07
PILOT APPLICATION TEMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 232
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100.0%; Pred. No. 2e-101;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                         Stewart, Timothy A
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Tumas, Daniel
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Gerritsen, Mary E.
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Watanabe, Colin K
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                       Beresini, Maureen
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Filvaroff, Ellen
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Filvaroff, Ellen
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Goddard, Audrey
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                                                DeForge, Laura
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RAPELICATION NUMBER: 60/086026

RELING DATE: 1998-06-04

RELING DATE: 1998-06-10

RELING DATE: 1998-06-10

RELING DATE: 1998-06-10

REPLING DATE: 1998-06-11

REPLING DATE: 1998-06-17

RELING DATE: 1998-06-17

REPLING DATE: 1998-06-18

RELING DATE: 1998-06-18

RELING DATE: 1998-06-19

REPLING DATE: 1998-06-23
                  R FILING DATE: 1998-05-13
R APPLICATION NUMBER: 60/085339
R FILING DATE: 1998-05-13
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R FILING DATE: 1998-05-15
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R APPLICATION NUMBER: 60/08597
R FILING DATE: 1998-05-15
R APPLICATION NUMBER: 60/086414
R FILING DATE: 1998-05-15
R APPLICATION NUMBER: 60/086414
R FILING DATE: 1998-05-12
R APPLICATION NUMBER: 60/086410
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R APPLICATION NUMBER: 60/090445
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090538
R FILING DATE: 1998-06-24
R FILING DATE: 1998-06-26
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R APPLICATION NUMBER: 60/091360
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APPLICATION NUMBER: 60/091982
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Best Local Similarity 100.
Matches 121; Conservative
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US-10-140-808-232
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 121; Conservative 0; Mismatches 0; Indels
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 232, Application US/10123904
Publication No. US20030022328A1
GENERAL INFORMATION:
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Smith, Victoria
Stewart, Timothy A.
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Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Filvaroff, Ellen
Gao, Wei-Qiang
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Gurney, Austin L.
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                                                                                                                    TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-232
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                                                                         SEQ ID NO 232
LENGTH: 189
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LENGTH: 189
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R.1060
CURRENT PILING DATE: US/10/140,470
CURRENT APPLICATION NUMBER: US/10/140,470
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: S50
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Job time : 133.055 secs
; Sequence 232, Application US/10140470; Publication No. US20030022331A1; GENERAL INFORMATION:
                                                                                                                                                                                                             Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
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Wood, William
                                                             Baker, Kevin P.
Beresini, Maureen
DeForge, Laura
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Filvaroff, Ellen
Gao, Wei-Qiang
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; ORGANISM: Homo Sapien
US-10-140-470-232
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APPLICANT:
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34568, A
4962, Ap
12686, A
4961, Ap
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34638, A
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                                                                                                  June 20, 2006, 05:01:19; Search time 12.7636 Seconds (without alignments) 334.012 Million cell updates/sec
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| EMC Celerra SIDS3/ptcdata/2/pubpaa/US09 NEW PUB.pep:*
| FMC Celerra SIDS3/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*
| FMC Celerra SIDS3/ptcdata/2/pubpaa/US07 NEW PUB.pep:*
| FMC Celerra SIDS3/ptcdata/2/pubpaa/NS08 NEW PUB.pep:*
| FMC Celerra SIDS3/ptcdata/2/pubpaa/PCT NEW PUB.pep:*
| FMC Celerra SIDS3/ptcdata/2/pubpaa/US08 NEW PUB.pep:*
| FMC Celerra SIDS3/ptcdata/2/pubpaa/US10 NEW PUB.pep:*
| FMC Celerra SIDS3/ptcdata/2/pubpaa/US11 NEW PUB.pep:*
| FMC Celerra SIDS3/ptcdata/2/pubpaa/US10 NEW PUB.pep:*
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189
1 MLGSRAVMLLLLLEWTAQGR......QAFVAVARVFAHGAATLSP 189
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-953-349-3458
US-10-953-349-34568
US-10-953-349-12686
US-10-953-349-12686
US-10-953-349-12686
US-10-953-349-12685
US-10-49-902-39265
US-10-49-902-39265
US-10-49-902-39265
US-10-953-349-12685
US-10-953-349-12684
US-10-953-349-12684
US-10-953-349-12684
US-10-953-349-12684
US-10-953-349-12684
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                                                                                                                                                                                                                                                                                                    96747 segs, 22556637 residues
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                                                                    - protein search, using sw model
                                                                                                                                                                                                                                                                     Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                       Run on:
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11785, A	11784, A	11783, A	363, App	3438, Ap	249, App	13, Appl	79, Appl	279, App	28491, A	39700, A	9223, Ap	29, Appl	11, Appl	73, Appl	35581, A	193, App	44672, A	33763, A	34641, A
Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence		Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-10-953-349-11785	US-10-953-349-11784	US-10-953-349-11783	US-10-538-066-363	US-10-471-571A-3438	US-10-538-066-249	US-11-257-581-13	US-11-154-977-79	US-09-949-925-279	US-10-449-902-28491	US-10-449-902-39700	US-10-953-349-9223	US-11-156-014A-29	US-10-518-472-11	US-11-154-977-73	US-10-953-349-35581	US-09-949-925-193	US-10-449-902-44672	US-10-449-902-33763	US-10-449-902-34641
653 6	662 6	684 6	702 6	818 6	10 6	16 7	26 7	29 1	40 6	40 6	44 6	47 7	48 6	•	57 6	58 1	9 09	9 99	77 6
7 3.7	7 3.7 6	7 3.7 (7 3.7	7 3.7 8	6 3.2	6 3.2	6 3.2	6 3.2	6 3.2	6 3.2	6 3.2	6 3.2	6 3.2	6 3.2	3.2	6 3.2	6 3.2	6 3.2	6 3.2
56	27	28	. 53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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RESULT 2
US-10-538-066-130

US-10-538-066-130

Sequence 130, Application US/10538066

Publication No. US20060094643A1

GENERAL INFORMATION:

APPLICANT: Bpimmune Inc.

TITLE OF INVENTION: HAA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen

TITLE OF INVENTION: HAA-A1, -B7, and -B44 Tumor Associated Antigen

TITLE OF INVENTION: Peptides and Compositions

FILE REPERSENCE: 2060.015PC06

CURRENT APPLICATION NUMBER: US 60/432,017

PRIOR APPLICATION NUMBER: US 60/432,017

PRIOR FILING DATE: 2002-12-10

NUMBER OF SEQ ID NOS: 767

SOPTWARE: PatentIn version 3.2
                                                                                                                                              -B7, and -B44 Tumor Associated Antigen
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                                                                                                               TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, TITLE OF INVENTION: Peptides and Compositions FILE REFERENCE: 2060.015PC06
CURRENT APPLICATION NUMBER: US/10/538,066
CURRENT FILING DATE: 2005-06-09
PRIOR PILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 767
SOFTWARE: PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.7%; Score 7; DB 6; Best Local Similarity 100.0%; Pred. No. 1.5; Matches 7; Conservative 0; Mismatches
                                         Sequence 129, Application US/10538066 Publication No. US20060094649A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT

ORGANISM: Homo sapiens

US-10-538-066-129
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RESULT 1
US-10-538-066-129
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LENGTH: 10
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LENGTH: 10
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Sequence 34638, Application US/10953349

Sequence 34638, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICATION TO TAXANDROV, NICKOlai et al.

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: US/10/953,349

CURRENT APPLICATION UNMERS: 105/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: Patentin version 3.3

SEQ ID NO 34638

LENGTH: 151
Sequence 39340, Application US/10449902
; Sequence 39340, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: National Institute of Physical and Chemical Research.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL.LENGTH PLANT CDNA AND USES THEREOF
; TITLE OF INVENTION: FULL.LENGTH PLANT CDNA AND USES THEREOF
; TITLE OF INVENTION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR FILING DATE: 2003-05-39
; PRIOR FILING DATE: 2002-05-30
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIN Ver. 2.1
; SEQ ID NO 33340
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Publication No. US20060088532A1
GENERAL INFORMATION:
APPLICANT: LOUGHG INStitute for Cancer Research et al., TITLE OF INVERTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION DATE: 2004-08-27
PRIOR FILING DATE: 2002-03-07
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100.0%; Pred. No. 17;
tive 0; Mismatches
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100.0%; Pred. No. 9.5;
iive 0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Oryza sativa
US-10-449-902-39340
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                                                                                                                                                                                                                                                                                                                                   Sequence 251, Application US/10538066
Publication No. US20060094649A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: HLA-Al, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
TITLE OF INVENTION: Peptides and Compositions
TITLE OF INVENTION: Peptides and Compositions
TITLE OF INVENTION Peptides and Compositions
CURRENT APPLICATION NUMBER: US/10/538,066
CURRENT FILING DATE: 2005-16-09
PRIOR PILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 767
SOFTWARE: Patentin version 3.2
SEQ ID NO 251
LENGTH: 11
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Publication No. US20060094649A1
GENERAL INFORMATION:
APPLICANT: Epimeune Inc.
TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, a
TITLE OF INVENTION: Peptides and Compositions
TITLE OF INVENTION: Peptides and Compositions
FILE REFERENCE: 2006.015PC06
CURRENT APPLICATION NUMBER: US/10/538,066
CURRENT FILING DATE: 2005-06-09
PRIOR APPLICATION NUMBER: US 60/432,017
PRIOR APPLICATION NUMBER: US 60/432,017
PRIOR APPLICATION NUMBER: US 60/432,017
PRIOR SEQ ID NOS: 767
SOOTWARE: Patentin version 3.2
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100.0%; Pred. No. 1.6;
tive 0; Mismatches
                                                                      Query Match 3.7%; Score 7; DB 6; Best Local Similarity 100.0%; Pred. No. 1.5; Matches 7; Conservative 0; Mismatches
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Matches 7; Conservative
; ORGANISM: Homo sapiens
US-10-538-066-130
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ORGANISM: Homo sapiens
US-10-538-066-251
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ORGANISM: Homo sapiens
US-10-538-066-252
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LENGTH: 11
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APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILLE REPERENCE: 2750-1579PUS2
CURRENT APPLICATION WUMBER: US/10/953,349
CURRENT APPLICATION WUMBER: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SEGTING DATE: 2004-09-30
SEQ ID NO 4961
LENGTH: 282
                                                                                                        APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT PILLORATION WUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 12686
LENGTH: 280
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: Bio-oriented Technology Research Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A20511-US
CURRENT APPLICATION NUMBER: US 200410449,902
CURRENT APPLICATION NUMBER: UP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2003-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-31
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100.0%; Pred. No. 29;
tive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches
                                          Sequence 12686, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
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; Publication No. US20060123505A1
; GENERAL INFORMATION:
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US-10-953-349-4961
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Best Local Similarity 100.
Matches 7; Conservative
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189 MLLLLLP 195
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US-10-449-902-39265
                       JS-10-953-349-12686
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APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VEFRION 3.3
SEQ ID NO 4962
LENGTH: 279
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Sequence 34563.

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROW, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERNINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

FILE REPRENCE: 2750-1579PUS2

CURRENT APPLICATION NUBBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: Patentin version 3.3

SEQ ID NO 34568
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100.0%; Pred. No. 29;
iive 0; Mismatches
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100.0%; Pred. No. 21;
tive 0; Mismatches
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100.0%; Pred. No. 26;
tive 0; Mismatches
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Publication No. US20060107345A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34568
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 100.0
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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NUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
SEQ ID NO 117
                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-117
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188 MLLLLLP 194
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US-10-953-349-34568
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US-10-953-349-4962
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| Publication No. US20060107345A1
| Publication No. US20060107345A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
| TITLE OF INVENTION: ENCONDED THERBY
| TITLE OF INVENTION: ENCONDED THERBY
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; Fublication No. US2006012305A1
; Fublication No. US2006012305A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-08
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT APPLICATION NUMBER: US 2002-203269
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR FILING DATE: 2002-05-30
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SCOFWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                              Query Match 3.7%; Score 7; DB 6; Best Local Similarity 100.0%; Pred. No. 30; Matches 7; Conservative 0; Mismatches
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 39265
LENGTH: 294
                                                                                                                                                               TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-39265
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; ORGANISM: Oryza sativa
US-10-449-902-37345
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239 MLLLLLP 245
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i Sequence 4960, Application US/10953349

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i TITLE OF INVENTION: ENCONDED THERRY

i TITLE OF INVENTION: ENCONDER: US/10/953,349

i CURRENT APPLICATION NUMBER: U
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